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GenCore version 5.1.6
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ROD 25-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a variety of vasoactive peptides J. Biol: Chem. 274 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi; Muridae; Murinae; Mus.
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                                                                                   Gaps
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Yokoyama,M. and Matsuo,M.
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                                           Length 2583;
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                                                                                                                                                                                                                                                                               Mus musculus soluble secreted endopeptidase delta mRNA.
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                                                                                   Indels
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Direct Submission
Submitted (08-JUN-1999) International Center for
                                                                                                                                                                                                                                                                                               alternatively spliced product, complete cds.
                                             DB 10;
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                                         Score 19.4; DE
Pred: No. 91;
0; Mismatches
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Pred. No. 91;
0; Mismatches
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Best Local Similarity 95.28;
Matches 20; Conservative
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Matches 20; Conservative
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LADNQMVNGFSTLGENIADNGGVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINY
AQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPMKRCR
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia: Rutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T., Iwatsubo, T. and Saido, T. C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases
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Mus musculus neprilysin-like peptidase alpha mRNA, complete cds. AF302075
Patent: WO 9953077-A 17 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS
CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME
MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
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Science Instititute, RIKEN, 2-1 Hirosawa,
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/db_xref="taxon:10090"
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/note="oligonucleotide"
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Shirotani, K. and Saido, T.C.
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illarity 100.0%; P
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351-0198,
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                         AF302076 2652 bp mRNA linear ROD 11-JUN-2001 Mus musculus neprilysin-like peptidase beta mRNA, complete cds.
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DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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Shirotani,K., Tsubuki,S., Iwata,N., Takaki,Y., Harigaya,W.,
Maruyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T.,
Iwatsubo,T. and Saido,T.C.
                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Instittute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
351-0198, Japan
                                                                                                                                                                                                                         Iwatsubo,T. and Saido,T.C.
Nebrilysin degrades both amyloid beta peptides 1-40 and 1-42 most
rapidly and efficiently among thiorphan- and
phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mus musculus neprilysin-like peptidase gamma mRNA,
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/organism="Mus musculus"
/db_xref="taxon:10090"
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Shirotani, K. and Saido, T.C.
Direct Submission
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PAT 07-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 2694)
Shirotani, K. and Saido, T.C.
Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKM
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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inhibitors useful in therapy
Patent: WO 9953077-A 1 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS
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                                                            1 (bases 1 to 2694)
Shirotani,K., Tsubuki,S., Iwata,N., Takaki,Y., Harigaya,W.,
Shirotani,K., Tsubuki,S., Kiyama,H., Iwata,H., Tomita,T.,
Maruyama,K., Kiryu-Seo,S., Kiyama,H., Iwata,H., Tomita,T.,
Iwatsubo,T. and Saldo,T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 rapidly and efficiently among filtently among filtently among filtently among filtently among thiorphan- and phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
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/product="neprilysin-like peptidase gamma"
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Pred. No. 91
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AX014701
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                                                                                                                                                                                                                        translation="MGKSESSVGMMERADNCGRRRLGFVECGLLVLLTLLLMGAIVTL
                                                                                                                                                                                                                                             GVFYSIGKOLPLLNSLLHVSRHERTVVKRVLRDSSOKSDICTTPSCVIAAARILQNMD
                                                                                                                                                                                                                                                                    QSKKPCDNFYQYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSSVQHRPA
                                                                                                                                                                                                                                                                                                          LNSOFNRRVLIDLFIWNDDONSSRHVIYIDOPTLGMPSREYYFKEDSHRVREAYLOFM
                                                                                                                                                                                                                                                                                                                               FSVATMLRRDLNLPGETDLVOEEMAOVLHLETHLANATVPOEKRHDVTALYHRMGLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKAYLOWLAGGRDORLPGLNLTYAQLFFINYAQVWCGSYRPEFAIQSIKTDVHSPLK
YRVLGSLONLPGFSEAFHCPRGSPMHPMNRCRIW"
                                                                                                                                                                                                                                                                                     VEKAKTLYRSCMNOSVIEKRDSEPLLNVLDMIGGWPVAMDKWNETMGPKWELERQLAV
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Yokoyama,M. and Matsuo,M.
Yokoyama,M. and Matsuo,M.
Molecular identification and characterization of novel
membrane-bound metalloprotease, the soluble secreted form of which
hydrolyzes a variety of vasoactive peptides
J. Biol. Chem. 274 (45), 32469-32477 (1999)
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Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
R); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME NTAL (FR); FACCHINETTI PATRICIA (FR)
LOCATION/Qualifiers
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/protein_id="AAF13152.1"
/db_xref="GI:6467399"
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Pred. No. 90;
                                                                                                                                            'note-"unnamed protein product"
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                                                                             /organism="Rattus rattus"
/db_xref="taxon:10117"
                                                                                                                                                                                /protein_id="CAC07576.1"
/db_xref="G1:10040976"
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'organism="Mus musculus"
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da, K., Emoto, N. and Matsuo, M.
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  CLAUDE (FR); O MARIE CHANTAL
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PAT 21-SEP-2000
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Patent: WO 0047750-A 12 17-AUG-2000;
BOILEAU GUY (CA) ; DESGROSEILLERS LUC (CA) ; UNIVERSTIE DE MONTREAL
                        DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQERFGLKG
FWWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTWQNYLVWRLVLD
                                                                         RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYNSNMESAVGSLYIKRAFSKDS
KSTVRELIEKIRSVFYDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
                                                                                                                                                     QIVFPÄGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDMMSN
FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSSLGENIADNGGVRQAYKAYLRMLA
                                                                                                                                                                                                        DGGKDORLPGLNLTTAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
LPGFSEAFHCPRGSPMHPMKRCRIW"
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FWYTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMONYLVWRLVLD
IDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKVRKAYPEFMTSVATMLRK
                                                                                                                                  DEEYSSLTFYEDLYFENGLONLKNNAQRSLKKLREKVDONLW1 IGAAVVNAFYSPNRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.4%; Score 19.4; DB 6; 95.2%; Pred. No. 90; Ative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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Sequence 12 from Patent WO0047750.
AX033272
                                                                                                                                                                                                                                                                                                                                        Score 19.4;
Pred. No. 90;
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/db_xref="Gi:10280088"
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Boileau, G. and Desgroseillers, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1220 CATCATGCCTTTTCTCCTGG 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CATCATGCTTTTTCTCTGGG 21
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                                                                                                                                                                                                                                                                                                                                        92.4%;
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Best Local Similarity 95.29
Matches 20, Conservative
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Best Local Similarity 95.2
Matches 20; Conservative
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norvegicus clone CH230-516, *** SEQUENCING IN PROGRESS ***
                                                         GI:17941511
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                                                                                                                                                                                       (bases 1 to 174953)
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                     unordered pieces.
                                                                                               Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submission
                                                                                                                  Rattus norvegicus
                                                                            HTG; HTGS PHASE1.
 DEFINITION
                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                       REFERENCE
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                                        ACCESSION
                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                AF176569 2925 bp mRNA linear ROD 11-MAY-2000 Mus musculus neprilysin-like metallopeptidase 1 (N11) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSTVRELIEKIRSVFVDNLDELNWMDEESKKKAOEKAMNIREOIGYPDYILEDNNKHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear HTG 20-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CMNQSVIEKRDSEPLLSVLKMVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-AUG-1999) Biochemistry, University of Montreal, 2900 Edouard Montpetit, Montreal, Que H3T 1J4, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              monse
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                  Ghaddar,G., Ruchon,A.F., Carpentier,M., Marcinkiewicz,M.,
Seidah,N.G., Crine,P., Desgroseillers,L. and Boileau,G.
Molecular cloning and blochemical characterization of a new mo
testis soluble-zinc-metallopeptidase of the neprilysin family
Biochem. J. 347 (Pt. 2), 419-429 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 2925)
Ghaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="neprilysin-like metallopeptidase 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ote="NL1; metallo-endopeptidase".
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Pred. No. 90;
0; Mismatches
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797 c 836 q 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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'tissue_type="testis"
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                                      1271 CATCATGCCTTTTCTCTGGG 1251
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                                                                                                                                                                                                                                                Mus musculus
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AF176569/c
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Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox.C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Coyle, M.D., Dang, Y., Dinh, H., Douthwaite, K.J., Delgado, O., Denber, H., Dugar-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferrauquo, D., Edwards, C.C., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunarathe, P., Hawes, T., Harnis, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Homeis, F., Howes, A., Houloway, C., Horlins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jally, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Angym;, rauser,..., vera,V., Villalon,D., Vinson, r., Ihomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson, r., Iall, R., Ward-Moore,S., Warren,R., Washington,C., Atlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Norlev,K., Wu,C., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                 Muzhy, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J. Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Borte, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burchell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shen, H., Shooshtari, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yauyan, w.yau, w. organye, N. oviedo, R., Pace, A., Payton, B.
yauh, M., Okwuon, G., Oganye, N., Oviedo, R., Primus, B., Pu, L.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.
4a,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
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dei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scott, G., Shen, H., Shooshtari;;
e.T., Sparks, A., Stanley, H.,
Jabor, P., Tamerisa, A., Tameriss
Taylor, T., Telfrod, B., Thomas, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rojubokan, I., Rolfe, M.
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fguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pickens, R., Primus, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 152255 bases at least 040 Consensus quality: 158448 bases at least 030 Consensus quality: 164461 bases at least 020
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.one,H., Sutton,A., Svatek,A., Tabor,P.
nng,H., Tansey,J., Taylor,C., Taylor,T.
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On Dec 20, 2001 this sequence ve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eery, J., Perez, L., Peters, L.,
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Estimated insert size: 155965; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
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AC126977 182933 bp DNA linear HTG 17-JUL-2002 Rattus norvegicus clone CH230-11A4, *** SEQUENCING IN PROGRESS ***, 78 unordered pleces.
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Consensus quality: 124341 bases at least 020

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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 78 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                NOTE: Estimated insert size may differ from sequence length
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                                                                                RS Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F. R., Allen, C. Ashbrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Babrand, J., Benton, J., Bluage, R., Blankenburg, K., Bonnin, D., Burkett, C., Burch, E., Burden, M., Bryant, N. P., Burden, J., Benton, J., Burkett, C., Burch, E., Burden, M. C., Carron, T. Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Claron, T. Carter, M., Cavazos, S. R., Chacko, J., Chavez, D., Chavez, D., Claron, C., Coyle, M. D., Dedharey, R. R., Delgado, O., Denn, A.L., Ding, Y. Dourbhaite, K. J., Draper, H. Dugan-Roche, S. P. David, R. Douthwaite, K. J., Draper, H. Dugan-Roche, S. Durbin, K. J., Dagar, D., Edwards, C. C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Elaggan, N., Ford, J., Garza, N., Gill, R., Barnhart, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Harris, R., Hube, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Joulah, S., Thue, J., Jackson, L. L., Li, J., Li, J., Liu, Y., Luin, Y., Luin, Y., Luin, R., Marinez, E., Manhiney, E., McLed, M., McHarin, R., Marinez, E., Mahnen, W., Mitcharge, O., Lieu, C., Liu, J., Liu, Y., Luin, Y., Luin, Y., Luin, Y., Luin, Y., Rorel, M., Morris, S., Moser, M., Netton, Y., Watton, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 182933)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
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On Jul 14, 2002 this sequence version replaced gi:21731393.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: GKAG
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Weinstock,G. and Gibbs,R.
                                                                      (bases 1 to 182933)
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2 (bases 1 to 182933)
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COMMENT

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Rattus norvegicus clone CH230-118C9, *** SEQUENCING IN PROGRESS ***, 75 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 25, 2002 this sequence version replaced gi:21627906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 170363).
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.
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                                                                                                                                                                                                                                                                                              Insert size: 208149; sum-of-contigs
Insert size: 219051; 2.3% error; agarose-fp
Quality coverage: 12.41x in Q20 bases; sum-of-contigs Quality
coverage: 12.08x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the apps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will * be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 others
                                                                                                                                                     Assembly program: XGAP4: version 4.5
Assembly program: XGAP4: version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: De-terminator; 11% of reads
Chemistry: Dye-terminator Big Dye; 88% of reads
Consensus quality: 207834 bases at least 040
Consensus quality: 207055 bases at least 040
Consensus quality: 208060 bases at least 020
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/note="assembly_fragment:01838
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BASE COUNT 54098 a 53647 c 51328 g 49076 t
                                                                                                                        ----- Project Information
                                                                                        Web site: http://www.sanger.ac.uk
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                                                                                                          Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-23".
1: .137303
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Rattus norvegicus
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Mus musculus chromosome 4 clone RP23-15L19, *** SEQUENCING IN
PROGRESS ***, 2 unordered pieces.
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Sciurognathi; Muridae; Murinae; Mus.
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Direct Submission
Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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Pred. No. 68;
0; Mismatches
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ò a consists of 75 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        site: http://www.hgsc.bcm.tmc.edu/
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Weinstock,G. and Gibbs,R.
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clone name: CH230-118C9

Center

Center project name: GSRJ

Summary Statistics

Sequencing vector: Plasmid;

bp in length length

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This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Bm:, EMBL; Sw:, GARSEROT: Tr:, TREMBL; WP:, WORMPEP: Information on the WORMPEP database can be found at
variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk/HGP/Chr10
RP11-69C17 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the entire insert of clone RPI1-69C17 The true left end of clone RPI1-35D13 is at 91113 in this sequence. The true right end of clone RPI1-35BN3 is at 80918 in this sequence. Location/Qualifiers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1PA7 repeat: matches 5572. .6143 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1MB6 repeat: matches 5529. .6179 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="HAL1 repeat: matches 1319. .1588 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note-"MLT1E repeat: matches 288. .519 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="HAL1 repeat: matches 63. .166 of consensus" 930. .4115 enote="MIR repeat: matches 47. .243 of consensus"
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note="MIR repeat: matches 23. .230 of
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Human DNA sequence from clone RPl1-69C17 on chromosome 10, complete
sequence.
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Where differences are found these are annotated as variations
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CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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During sequence assembly data is compared from overlapping
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LOCUS

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AP000275 74600 bp DNA linear PRI 20-NOV-1999 Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone: 11866, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to. 74600)

Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.

Homo sapiens 74,600bp genomic DNA of 21q22.1

Published Only in DataBase (1999)

2. (bases 1 to 74600)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555
                                            consensus
    1. .306 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                        .312 of consensus'
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Pred. No. 1.18+02;
0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="38 copies 4 mer gtgt 67% conserved" 38760. .38899
                            5166. .35515
note="MLTIAl repeat: matches 3. .362 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="30 copies 2 mer gt 71% conserved"
8720. 38889
note="5 copies 34 mer 68% conserved"
                                                                                                                                                                                                                                                                          note="13 copies 21 mer 73% conserved". 36568
                                                                                                                                                                                                                                                                                                                                                         13 copies 22 mer 71% conserved".36560
                                            16242. .36565 ----- maccnes 3. .362
fnote="6 copies 54 mer 71% conserved"
6282. .36567
                                                                                                                                                                                                note="8 copies 34 mer 76% conserved"
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note-"5 copies 53 mer 74% conserved"
16300. 36572
                                                                                                                                                                                                                                                                                                                   note="3 copies 88 mer 84% conserved"
                                                                                                                                                                                                                                                                                                                                                       note="9 copies 28 mer 77% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8725. .38900
note="8 copies 22 mer 65% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18724. .38883.
/note="4 copies 40 mer 71% conserved"
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      repeat: matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     745.7.1001

1016--11M1 repeat: matches 5800. 6300 of consensus"

1018--21137

1016--11MA1 repeat: matches 5707. 5806 of consensus"

1016--MADE1 repeat: matches 4. 80 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ote-"LTRIGA repeat: matches 120. .430 of consensus" 862. .27101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /394. 27709
note="WLTIC repeat: matches 132. .462 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ote="AluSq/x repeat: matches 1. .133 of consensus" 178. .24494 ote="AluSx repeat: matches 1. .307 of consensus"
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'note-"MLTIC-internal repeat: matches 542. .650 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSc repeat: matches 1. .235 of consensus"
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note="MLTIC repeat: matches 1. .458 of consensus"
0624. .30978
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440. .17605
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827. .19907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .88 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 copies 5 mer tatat 57% conserved".7088
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note="MLTIC-internal repeat: matches 1126.
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                                                                                                                                                                                                                                                                                                                                                                                                              copies 4 mer acac 97% conserved"
                                                                                                                                                                                                                                                      copies 2 mer aa 76% conserved"
                                                                                                                                                                                                                                                                                                                                                                         copies 2 mer ga 76% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ote="26 copies 2 mer aa 71% conserved"
513. 25804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  copies 139 mer 87% conserved"
                                                                                                                                                                                                                                                                                                                             copies 28 mer 92% conserved"
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lote="2 copies 37 mer 93% conserved"

1067. .27226

lote="4 copies 40 mer 86% conserved"
                                                                                    5 copies 34 mer 69% conserved".13200
                  mer 75% conserved"
                                                        conserved"
                                                                                                                                                                           copies 53 mer 67% conserved"
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39. .17439
                                                        mer 85%
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The sequencing project is supported by Japan Science Technology Corporation (JST) and The Institute of Physical and Chemical Research (RIKEN).

1. 74600

7.01ganism="Hamon sapiens"

7. 750mism="Laxon: 9606"

7. 750mism="12"

7.
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87.6%; Score 18.4; DB 9; Length 74600;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                             FEATURES
Source
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ORIGIN
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Gaps

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Search completed: July 8, 2003, 03:35:03 Job time: 235.102 secs

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OM nucleic - nucleic search, using sw model

8, 2003, 00:43:28

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Run on:

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Human immune/haema
Human snare YKT6 g
Human ORF3687 cDNA
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Human nervous syst
                                                                                                 Human endometrium
Human secreted pro
Human polynucleoti
                                                                                                                                                                             Hydrophobic domain
Human PACAP genomi
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Bacillus subtilis
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DNA encoding novel
DNA encoding novel
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                       Human cervical can
Tet-07/MMP13* tran
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Human ORFX ORF1389
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                                                  Human matrix metal
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Human matrix meta]
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                                                                         Human EST-derived
Hydrophobic domai
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                                                                                                                                       secreted
                                                                                                                                        luman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat membrane metalloprotease NEPII gene probe #13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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AAX19486.
AAV84607
ABA83390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98FR-0004389.
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 71
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123219
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Schwartz JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                RESULT 1
AAZ28823
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Human T lymphocyte
Human polynucleoti
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                                                                                                     (without alignments)
358.431 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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/SIDS2/gcgdata/geneseg/genesegn-emb1/NA2001B.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gogdata/geneseq/geneseqn-embl/NA1984.DAT:*/SIDS2/gogdata/geneseq/geneseqn-embl/NA1985.DAT:*/SIDS2/gogdata/geneseqy-eneseqn-embl/NA1985.DAT:*/SIDS2/gogdata/geneseqy-eneseqn-embl/NA1987.DAT:*/SIDS2/gogdata/geneseq/geneseqn-embl/NA1987.DAT:*/SIDS2/gogdata/geneseq/geneseqn-embl/NA1987.DAT:*/SIDS2/gogdata/geneseq/geneseqn-embl/NA1988.DAT:*
                                                                                         ; Search time 131.941 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ogdata/geneseq/geneseqn-embl/NA1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995
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/SIDS2/gcgdata/geneseg/genesegn-emb1/NA1981.
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_101002:*

Database

/SIDS2/9

2185239 seqs, 1125999159 residues

21

catcatgctttttctcctggg. Gapop 10.0 , Gapext 1.0

Scoring table:

Searched:

US-09-647-780A-17 21 1 catcatgetttter

Perfect score:

Title:

Sequence:

WPI; 1999-593429/51

Human polynucleoti Human matrix metal

AAD28130 AAZ28810 AAA63763 AAS64388 AAH79862 AAQ28175 ABL91759

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AAZ28823

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Query Match

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Result Š

SUMMARIES

purified nucleic acid

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Disclosure, Fig 6, 167pp; English.
                    The invention relates to
                                                                                                                                                                                                                                                                                                                                                                                                          neuron;
                                                                                                                                                                                                                                                                                             AAZ28810/c
                                                                                                                                                                                                                                                                                                                                                                                              Rat;
                                                                                                                                                                                                                                                                                RESULT 3
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                                                                                                                                                                                                                                                                                                                            SXE
                                                                                                                                                                                                                                                                                                                                                           Sequences AA228811-228827 represent probes for detecting the rat membrane metalloprotease designated neprilysine II (NEPII) gene (AA228810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic- hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as
                                                                                                                                                                                                                                                                                                                                                                                                                                          analgesic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme; gynaecological; antisense-therapy; male erectile dysfunction;
MED; female sexual dysfunction; FSD; female sexual arousal disorder;
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phillips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 soluble
             οĮ
           New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardiovascular disease
                                                                                                                                                                                                                        Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEP; endocrine; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated and/or purified nucleic acid encoding a human
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wayman CP,
                                                                                                                                                                                                                                                                                                                                                                                                                   Soluble secreted endopeptidase (SEP) consensus DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1664..2286
/*tag= a
/note= "Encodes catalytic domain"
                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wayman CP,
                                                                                                                                                                                                                100.0%; Score 21; DB 2
1 Similarity 100.0%; Pred. No. 2.4;
21; Conservative 0; Mismatcher
                                                                                                                                                                                                   Sequence 21 BP; 2 A; 6 C; 4 G; 9 T; 0 other;
                                                                                                                                                                                                                                                                    21,
                                                                                                                                                                                                                                                                               1 CATCATGCTTTTCTCCTGGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT,
                                                                                                                                                                                                                                                                                                                                                  BP.
                                                       Claim 3; Page 23; 29pp; French.
                                                                                                                                                                                                                                                                     1 CATCATGCTTTTTCTCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                         endopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     female sexual arousal disorder
                                                                                                                                                                                                                                                                                                                          RESULT 2
AAD28130/c
ID AAD28130 standard; DNA; 2286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUL-2000; 2000GB-0017387
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stacey P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-155042/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200206492-A1
                                                                                                                                                                                                                                                                                                                                                                                             07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus sp.
Rattus sp.
                                                                                                                                                                                disorders
                                                                                                                                                                                                                                                                                                                                                                       AAD28130;
                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSAD;
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ö
                                                                                                                                                                                                                            as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and appoactive sexual desire disorder. The present sequence is SEP consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       designated neprilysine II (NEPII), which is involved in (In)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or
                                                                                                                                                              (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metalloprotease
encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane metalloprotease; neprilysine II; NEPII; inactivation;
on; hormone; peptide messenger; inhibitor; detection; disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular disease; neurodegenerative disease; growth disorder. hypothalamic-hypophyseal axis; endocrine disorder; ds.
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to screen for inhibitors,
cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                              Length 2286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonhomme MC, Facchinetti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the gene for the rat membrane
                                                                                                                                                                                                                                                                                                                                                       Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INRM ) INSERM INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                              Score 19.4; DE
Pred. No. 25;
0; Mismatches
                                                                                                                                                                                                                                                                                         ONA sequence found in human, mouse and rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat membrane metalloprotease NEPII gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New membrane metalloprotease NEP II, neuronal and hormonal peptides, used potentially useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             945 CATCATGCCTTTCTCTGGG 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ28810 standard; cDNA; 2765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haret C,
                                                                                                                                                                                                                                                                                                                                                                                                                     92.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.2%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gros C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAY44177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schwartz JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouimet T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . AAZ28810;
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Length 2925;

DB 21;

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Query Match
Best Local Similarity
Query Match
Best Local Simi
Matches 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes a murine neutral endopeptidase metallopeptidase-like enzyme, designated NL-1. The specification also describes NL-2 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimmeric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "neutral endopeptidase metallopeptidase-like enzyme NL-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neprilysin; neutral endopeptidase metallopeptidase-like enzyme; NEP-like enzyme; protein production; protein secretion; neurological disease; Alzheimer's disease; pain; psychiatric disorder; fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. Nt enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1.
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
                                                                   Length 2765;
                                                                                                                ö
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;
                             Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;
                                                                   Score 19.4; DB 20;
Pred. No. 25;
                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
332..2629
                                                                                                                                                                                   1073 CATCATGCCTTTTCTCCTGGG 1053
                                                                                                                                                          1 CATCATGCTTTTTCTCCTGGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3; 59pp; English.
                                                                                                                                                                                                                                                                                            763/c
AAA63763 standard; cDNA; 2925 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         processing by the NL-3 enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desgroseillers L, · Boileau G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99CA-2260376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-2000; 2000WO-CA00147.
                                                                     ch 92.4%;
1 Similarity 95.2%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product=
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYMO-) UNIV MONTREAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-549148/50.
P-PSDB; AAB08130.
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200047750-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                         AAA63763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                    Matches
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              printed
from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded polypeptides, useful in oping, identification of mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ilagnostics, forensics, gene mapping, identification of mutation esponsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not appear in the fication, but was obtained in electronic format directly
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the invention relates to isolated polynucleotide (I) and
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1804 BP; 441 A; 465 C; 433 G; 465 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding novel human diagnostic protein #192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                           Mismatches
Score 19.4; 1
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 192; 103pp; English.
                                                                                                                                                      1271 CATCATGCCTTTCTCCTGGG 1251
                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and
                                                              ö
                                                                                                                          1 CATCATGCTTTTTCTCTGGG
                                                                                                                                                                                                                                                                                                                                         AAS64388 standard; cDNA; 1804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
   92.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002 (first entry)
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification, but
                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABG00201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnostics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                  AAS64388;
                                                                                                                                                                                                                                                                                                             AAS64388/c
                                                                                                                                                                                                                                                                                    RESULT 5
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Score 17.8; DB 23; Length 1804; Pred. No. 1.3e+02;

84.8%; 90.5%;

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Gaps

Length 51;

Score 17.4; DB 22; Pred. No. 1.2e+02;

82.98;

Mismatches

; ; 21

18; Conservative

Query Match Best Local Similarity Matches 18; Conserv

3 TCAIGCTTTTTCICCIGG

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4-hydroxybutyrate; dehydrogenase; protein therapy; adenosine triphosphate-dependent RNA helicase; major histocompatibility antigen; MHC; major histocompatibility complex Class I histocompatibility antigen; MHC; phosphoglycerate kinase; immunosuppressive; immunostimulatory; antisclerotic; antidiabetic; antilifiammatory; cytostatic; antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphic variants of proteins (AAG98010-AAG98238) related to anglopoletin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP) dependent RNA heliacase, major historompathility complex (MHC) class I historompathility antigen and/or phosphoglycerate kinase. These nucleic acid single nucleotide polymorphisms (SNPs) and the encoded antirheumatic, have potential immunosuppressive, immunostimulatory, cytostatic, antirheumatic, antisclerotic, antidiabetic, antinilammatory, cytostatic, antileukemic, neuroprotective and antimicrobial activity and may be useful in gene/protein therapy, vaccines, modulation of the expression and activity of proteins related to angiopoletin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate (ATP)-dependent RNA halicase, major histocompatibility complex (MHC) class I histocompatibility antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      histocompatibility antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erytheromatosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system, an infection of pathogenic organisms. They may also be used to alter phenotypic traits such as longevity, appearance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic nucleic acids encoding e.g. anglopoietin, dehydrogenase, adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosed and/or treated by the above methods include multifactorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases with a genetic component, such as autoimmune diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding
                                                                                                                                                                                                                                                                                                     Human DNA containing single nucleotide polymorphism SEQ ID NO. 477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetes, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and/or phosphoglycerate kinase. Disorders that may be prevented
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AAH79386-AAH80036)
                                                                                                                                                                                                                                                                                                                                              Human; single nucleotide polymorphism; SNP; anglopoletin;
    Indels
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6
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to nucleic acids
                                                             1255 CATCCTGCTTTGTCTCCTGGG 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 193; 484pp; English.
                                        1 CATCATGCTTTTTCTCCTGGG 21
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                                                                                                                                                                               AAH79862 standard; DNA; 51 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strength, speed and endurance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-DEC-2000; 2000WO-US35346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0472688.
                                                                                                                                                                                                                                                               (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-418297/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200148245-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimkets RA,
                                                                                                                                                                                                                                                               19-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2001
19;
                                                                                                                                                                                                                       AAH79862;
Matches
                                                                                                                                           RESULT
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RNA was isolated from peripheral lymphocytes and converted to cDNA using a C-beta-specific primer. The CDNA was amplified by anchored PCR using C-beta and polyc primers, then amplified again using a different C-beta specific primer. The amplified product was Saciir restricted, inserted into Bluescript SK+ vector and used to transform F.coll XL-lblue. Transformants were screened with a C-beta specific probe and DNA from positive clones was sequenced in the C-beta region. The sequence designated "IGR D 04" is a consensus sequence from 4 distinct cDNA clones, as was seen at position 154 in place of a A and an A at position 160 instead of a G. The sequence has an homology of 75.7% with the sequence VB12A1 (see Leiden J.M., et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11., Proc.Natl. Acad. Sci. USA, 83:4456, 1986) but has a homology of less than 75% with other members of the Vbeta 5 subfamily. IGR b 04 is, therefore, not a member of the Vbeta 5 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Variable regions of b-chain of T-lymphocyte receptors and their DNA - useful as immuno:modulant(s) and for diagnosing immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.4; DB 13; Length 329;
Pred. No. 1.6e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                         TCR; V beta w23 subfamily; variable region; anchored PCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triebel F;
                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "encodes a V beta segment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 329 BP; 83 A; 92 C; 75 G; 79 T; 0 other;
                                                                                                                                                                                                                       Human T lymphocyte receptor V-region "IGR b 04"
                                                                                                                                                                                                                                                                             polymerase chain reaction; T cell receptor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hercend T, Roman-Roman S,
                                                                                                     AAQ28175 standard; cDNA to mRNA; 329 BP.
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
18..329
29 TCATGCTTTGTCTCCTGGG: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 39; 75pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-FR00130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91FR-0001613.
91FR-0004523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.78;
                                                                                                                                                                                11-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ROUS ) ROUSSEL-UCLAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-300036/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See AAQ28173-Q28228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR26962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferradini L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-1992;
                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1991;
12-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                W09213950-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                      AAQ28175
               a
a
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Gaps

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Conservative

Sequence 51 BP; 8 A; 17 C; 13 G; 13 I; 0 other;

RESULT 8 **ABL91759**

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The present invention provides the cDNA, protein and gene fragments of the human matrix metalloproteinase 13 (collagenase 3) (MMP13). Also provided are single nucleotide polymorphisms (SNPS) identified within the sequences. The sequences can be used to haplotype an individual and in the treatment of cancer and arthritis, including metastatic cancers. The present sequence is one version of the MMP13 cDNA, the gene for which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The present sequence is stated as being the same as that shown as SEQ ID NO: 4 in the sequence listing of the specification. However, the sequences differ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel genetic variants of matrix metalloproteinase 13 (collagenase 3) gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. cancer and arthritis -
                                                                                                                   arthritis; haplotype; single nucleotide polymorphism; SNP; enzyme; cytostatic; antiarthritic; gene therapy; chromosome 11q22.3; gene; ss
                                                                                           matrix metalloproteinase 13 (collagenase 3); MMP13; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.4; DB 24; Length 1416;
Pred. No. 1.9e+02;
); Mismatches 1; Indels 0;
                                       Human matrix metalloproteinase 13 (collagenase 3) cDNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1416 BP; 388 A; 328 C; 307 G; 393 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanguay. DA
                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Messer C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; Fig 4; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TCATGCTTTTTCTCTGGG 21
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                                                                                                                                                                                                                                                                                                                                                                                                      replace(1080,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
replace(1169,G)
                                                                                                                                                                                                                                                                                                                          /product= "MMP
replace(326,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 82.9%;
1 Similarity 94.7%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-2000; 2000US-217950P.
17-AUG-2000; 2000WO-US22693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JUL-2001; 2001WO-US22238
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  (first entry)
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                                                                                                                                                                                                                                                                        1..1416
/*tag= 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-171797/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAM48977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200206294-A2
                                                                                                                                                                                                       Homo sapiens
03-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                         allele
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AAX90499
ID AAX90.
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AC AAX90
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DT 04-OC
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                                                       FFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, ild, develomental or prinon-genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases
                                                                                                                                                                                                                                                                                                                                                                                    Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating tumors, having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 82.9%; Score 17.4; DB 24; Length 1416; Local Similarity 94.7%; Pred. No. 1.9e+02; hes 18; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting gene expression in cells, useful for e.g. treating by introducing double-stranded complementary oligoRNA having terminal bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1416 BP; 389 A; 328 C; 306 G; 393 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stability and thus intracellular concentration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hadwiger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 75-76; 104pp; German.
                                                                                                                                                                                                                                                                                                                                    Human polynucleotide SEQ ID NO 102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL44663 standard; cDNA; 1416 BP
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                                       16 TCATGCTTTGTCTCCTGGG 34
                                                                                                                                                                                       ABL91759 standard; DNA; 1416, BP
             TCATGCTTTTTCTCTGGG 21
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                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RIBO-) RIBOPHARMA AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-270454/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens.
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Gaps

Matches

δ g AAL44663 ID AAL4 XX AC AAL4 XX

RESULT 9

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P-PSDB; AAB84616.
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                                                                                              Homo sapiens
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                                                                                                                                            Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes transgenic mammals that express secondinant matriar-degrading enzymes (MDE) in a temporally and spatially regulated manner. The transgenic mammals produce phenotypic changes associated with cartilage-degenerative disease if maintained under conditions in which the recombinant gene is selectively expressed in joint tissue. The transgenic animal models are useful for determining the potential of a composition to counteract cartilage-degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease. The present sequence encodes human matrix metalloproteinase 13 (MMP-13) which can be used as the recombinant MDE in a transgenic
                                                Human; matrix metalloproteinase 13; MMP-13; collagenase 3; cartilage;
degenerative disease; matrix degrading enzyme; MDE; transgenic mammal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.4; DB 20; Length 1521; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transgenic mammals that express recombinant matrix-degrading enzymes, used to study phenotypic changes associated with cartilage-degenerative disease
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                                                                                                                                                                                                                                                                     /product= "MMP-13"
/note= "matrix metalloproteinase"
Human matrix metalloproteinase 13 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                           Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 1B-1C; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TCATGCTTTTTCTCCTGGG 21
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ilarity 94.7%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0068312.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Killar LM, Neuhold LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-468690/39.
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAY29419
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                               W09931969-A2
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19-DEC-1997;
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The specification describes a pharmaceutical composition, comprising a growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent, i.e. a protease. The inhibitor agent in a growth factor, that is upregulated in a damaged tissue such as a wound environment. Growth factors which are included in the composition of the invention are platelet-derived growth factor (PGF), fibroblast growth factor (FGF), connective tissue derived growth factor (CTGF), farathnocyte-derived growth factor (KGF), transforming growth factor (GFF), connective drowth factor (KGF), transforming growth factor (GFF), and chrysalin. Inhibitors which are included in the composition of the invention include inhibitors of urokinase-type plasminogen activator (UPA) and matrix metalloproteinase (MMP). The composition is useful for the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers. The present sequence encodes a human construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition for the treatment of damaged tissue i.e. chronic wounds and dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
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granulocyte macrophage colony stimulating factor; GM-CSF; uPA; vascular endothelial growth factor; urokinase plasminogen activator; dermal ulcer; wound; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Pred. No. 2.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cervical cancer marker nucleic acid 3882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 561-562; 572pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcintosh FS,
                                                                                                                                                                                                                 Location/Qualifiers
5.1420
/*tag= a
/product= "MMP-13"
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-2000; 2000WO-IB01935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davies MJ, Huggins JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-418351/44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
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The present invention describes transgenic mammals that express recombinant matrix-degrading enzymes (MDE) in a temporally and spatially regulated manner. The transgenic mammals produce phenotypic changes associated with cartilage-degenerative disease if maintained under conditions in which the recombinant gene is selectively expressed in joint tissue. The transgenic animal models are useful for determining the potential of a composition to counteract cartilage-degenerative disease. The present sequence represents a transgene with a tet07 promoter driving expression of a constitutively active human MMP-13 protein followeb by an SV40 splice and polyadenylation signal, where the transgene is designated Tet-07/MMP13*.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="this sequence contains introns. no stop codon"
020..4139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; matrix metalloproteinase 13 (collagenase 3); MAP13; cancer; arthritis; haplotype; single nucleotide polymorphism; SNP; enzyme; cytostatic; antiarthritic; gene therapy; chromosome 11q22.3; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human matrix metalloproteinase 13 (collagenase 3) gene fragment #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.4; DB 20; Length 2792;
Pred. No. 2.10+02;
0; Mismatches 1; Indels 0;
                                                                                               Transgenic mammals that express recombinant matrix-degrading enzymes, used to study phenotypic changes associated with cartilage-degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2792 BP; 814 A; 598 C; 601 G; 779 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
4020.10699
/*tag= b
/product= "MMP13 fragment"
                                                                                                                                                                                       Example 3; Page 63-64; 70pp; English.
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replace(3915,G)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1059 TCATGCTTTCCTCGGG 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL45714 standard; DNA; 11495 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TCATGCTTTTTCTCCTGGG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eplace(4437, T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.9%;
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474..5118
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                 Neuhold LA;
                                                           WPI; 1999-468690/39
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                   Killar LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL45714;
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The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded copypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; matrix metalloproteinase 13; MMP-13; collagenase 3; cartilage; degenerative disease; matrix degrading enzyme; MDE; transgenic mammal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 94.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2753 BP; 857 A; 523 C; 557 G; 806 T; 10 other;
                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                        Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 757-758; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              615 TCATGCTTTTCCTCCTGGG 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX90501 standard; DNA; 2792 BP
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97US-0068312
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2000US-0189315
                                                                                                                                08-DEC-2000; 2000WO-US33312
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2000US-0210600
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                                                                                                                                                                                                                                                                                                                                                                        Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-375006/39.
                                              WO200142467-A2
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19-DEC-1997;
      Homo sapiens
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21-JUL-2000;
                                                                                                                                                                                                  21-DEC-1999;
14-MAR-2000;
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                                                                                        14-JUN-2001
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Sequence 11495 BP; 3577 A; 2093 C; 1948 G; 3803 T; 74 other;
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AAI93579/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel genetic variants of matrix metalloproteinase 13 (collagenase 3) gene useful in studying expression and function of the protein, and for screening drugs to treat diseases e.g. cancer and arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the cDNA, protein and gene fragments of the human matrix metalloproteinase 13 (collagenase 3) (MMP13). Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence is a fragment of the MMP13 gene, which is found on chromosome 11q22.3.
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                                                                                                                                                                                                     splace(5290,G)
 /*tag= h
replace(5037,G)
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splace(5363,A)
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                                                     eplace(5102,G)
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number= "5"
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9616..10565
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0566..10699
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17-AUG-2000; 2000WO-US22693
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500..9615
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P-PSDB; AAM48977.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoiesis regulating activity, issue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
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                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. Leukaemia, inflammation and immune disorders
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      Length 11495
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                                                                 Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Ouery Match 82.9%; Score 17.4; DB 24; Best Local Similarity 94.7%; Pred. No. 2.5e+02; Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 16.8; DB 22;
90.0%; Pred. No. 3e+02;
ive 0; Mismatches 2;
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                                                                                                                                                                 5490 TCATGCTTTTCCTCGG 5508
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                                                                                                                                   3 TCATGCTTTTTCTCCTGGG 21
                                                                                                                                                                                                                                                                                                                                                         AAI93579 standard; cDNA; 406 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0515126
2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0%
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56.
P-PSDB; AA013648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo saptens.
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18-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001.
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qq

Search completed: July 8, 2003, 02:19:10 Job time : 133.941 secs Appl

Sequence 32, Sequence 104 Sequence 1, Sequence 3, Sequence 3, Sequence 3, Sequence 2, Sequence 97, Sequence 97, Sequence 97, Sequence 97,

Sequence 3, Al Sequence 33, 1 Sequence 33, 1 Sequence 115, Patent No. 543

Sequence

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APPLICANT: HERCEND, THIERRY; TRIEBEL, FREDERIC;
APPLICANT: ROMAN-ROMAN, SERGIO; FERRADINI, LAURENT
TITLE OF INVENTION: WARLENDES EBOUENCE CODING FOR
TITLE OF INVENTION: VARIABLE REGIONS OF BEPA CHAINS OF HUMAN T LYMPHOCYTE
TITLE OF INVENTION: RECEPTORS, CORRESPONDING PEPTIDE SEGMENTS AND THE
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES
                                                                          US-09-615-192A-33
US-09-615-192A-115.
                                                                                                                                                                                                                                                                                                                                                        PCT-US96-06352-97
PCT-US96-06583-97
                                                                                                                                              US-09-288-143-32
                                                                                                                                                                   US-09-227-357-10
US-09-045-186-1
US-09-045-186-3
                                                                                                                                                                                                                                                               US-09-413-068-3
US-09-403-345A-3
                                                                                                                                                                                                                                                                                                             PCT-US93-05039-2
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                                                                                                                                                                                                                                         US-09-413-452-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,530
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: PCT/FR92/00130
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR/91/01613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/423,383
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FR/91/04523
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 146.11!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08423383
Patent No. 5700907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 12-FEB-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: NEW YORK STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                               8, 2003, 01:24:03 ; Search time 28.9902 Seconds (without alignments) 222.151 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               escription
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/RE_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-404-879A-79
-09-404-879A-253
-09-404-879A-254
                                                                                                                                                                                                                                                                                                                                                                                                                                          of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                            441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                           1 catcatgctttttctcctggg 21
                                                                                                                                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                   US-09-647-780A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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Total number

Searched:

Sequence:

Run on:

TELECOMMUNICATION INFORMATION

212-661-8000

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTIC

Sequence

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GENERAL INFORMATION:
APPLICANT: Micham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462c2
CURRENT PELLING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FASTSEQ for Windows Version 3 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: ODPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REPERBENCE: 21012.46202
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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                                                                                                                                                                                                                                          Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15.8; DB 4;
Pred. No. 1.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                        82.9%; Score 17.4; 94.7%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 253, Application US/09404879A Patent No. 6468546
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-404-879A-79
Sequence 79, Application US/09404879A
Patent No. 6468546
; GENERAL INFORMATION:
                                                                                                ORGANISM: HUMAN
CELL LINE: HUMAN T LYMPHOCYTE
                                                                                                                                                                           ; OTHER INFORMATION: V BETA W23 US-08-437-353A-4
                                                                                                                                                                                                                                                                                                                      3 TCATGCTTTTTCTCCTGGG 21
                                                                                                                                                                                                                                                                                                                                          16 TCATGCTTTGTCTCCTGGG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CATCATGCTTTTTCTCCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 CAGCATGCTCTTCTCCTG
                                      TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA TO MRNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.2%;
                                                                                                                                                                                                                                                                                 Conservative
                        DOUBLE
                                                                                                                                                             NAME/KEY: IGR D'04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo saplen
US-09-404-879A-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapien US-09-404-879A-253
    NUCLEOTIDE
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-404-879A-253/C
                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ
SOFTWARE: Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 79
LENGTH: 226
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LENGTH: 226
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    TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEGMENTS AND THE DIAGNOSTIC
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                    Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HERCENO, THIERRY; TRIEBEL, FREDERAL,
APPLICANT: ROMAN, SERGIO; FERRADINI, LAURENT
APPLICANT: ROMAN, NUCLEOTIDE SEQUENCE CODING FOR
TITLE OF INVENTION: VARIABLE REGIONS OF BETA CHAINS OF
TITLE OF INVENTION: RECEPTORS, CORRESPONDING PEPTIDE SF
TITLE OF INVENTION: AND THERAPEUTIC USES
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                    Score 17.4;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/934,530
FILING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00130
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,353A
FILING DATE: 09-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATE:
APPLICATION DATA:
APPLICATION NUMBER: FR/01/CFILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/423,383
FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08437353A Patent No. 5830758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5: BIERMAN & MUSERLIAN
600 THIRD AVENUE
                                                                                                                                      ) NAME/KEY: IGR b 04
) OTHER INFORMATION: V BETA W23
US-08-423-383-4
                                                                                                  HUMAN T LYMPHOCYTE
                                                                                                                                                                                                                                                                                                    3 TCATGCTTTTTCTCCTGGG 21
                                                                                                                                                                                                                                                                                                                        16 TCATGCTTTGTCTCCTGGG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: CHARLES A. MUSERLIAN REGISTRATION NUMBER: 19,68
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA TO MRNA
ORIGINAL SOURCE:
ORIGINASM: HUMAN
                                                                                                                                                                                                                  Ouery Match 82.9%;
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-661-800
INFORMATION FOR SEQ ID NO
SEQUENCE CHARACTERISTIC
LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10016
                                                                                                  CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-437-353A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Gaps

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Length 513;
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                                                                                                                                                                                                                                                                                                                                    Score 15.4; DB 3;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 240/247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: September 13, 199
APPLICATION NUMBER: 60/009,102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/714,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49, Application US/09265315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                  386 ATCATACTTTNCTCCTG 403
                                                                                                                                                                                                                                                                                                                                                                                                               2 ATCATGCTTTTTCTCCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/
FILING DATE: March 9, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malouin, Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
                                                       NAME: Warburg, Richard J.
REGISSRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22
RELECOMMUNICATION INFORMATION
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (213) 489-1600
                                                                                                                                                                     TELEX: 67-3510
NFORMATION FOR SEQ ID NO: 49
SEQUENCE CHARACTERISTICS:
                                                                                                                             (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Warburg, Richard
                                                                                                                                                                                                                      LENGTH: 513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 88.5
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee, Ving J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 90071-2066
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US-08-714-918-49
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                                                                                                                                                      TELEFAX:
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                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                              Gaps
                                                                                                                                                                                                                                         APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: LAGGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 333
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sun, Dongxu-,
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
                                Indels
           Best Local Similarity. 89.5%; Pred. No. 1.1e+02; Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 15.8; DB 4;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
SYSTEM: IBM P.C. DOS 5.0
Word Perfect 5.1
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September 13, 1996
                                                                                                                                                                                               Sequence 254, Application US/09404879A Patent No. 6468546 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: 60/009,102
December 22, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 49, Application US/08714918 Patent No. 6037123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EE: Lyon's Lyon
633 West Fifth Street
Suite 4700
                                                                                        199 CAGCATGCTCTTTCTCCTG 181
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                                                                     1 CATCATGCTTTTTTCTCCTG 19
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Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 75.2
Best Local Similarity 89.5
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapien
US-09-404-879A-254
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                   -09-404-879A-254
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 254
LENGTH: 226
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                                                     Length 513;
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                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHODS OF SCREENING FOR COMPOUNDS ACTIVE ON STAPHYLOCOCCUS AUREUS TARGET GENES
                                                Score 15.4; DB 4;
Pred. No. 1.9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.4; DB 4;
Pred. No. 1.9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714 918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/266,417
FILING DATE: March 9, 1999
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Marlouin, Partrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Such Dongxu
TITLE OF INVENTION: METHODS OF ST
TITLE OF INVENTION: ACTIVE ON STA
TITLE OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: SALLE 4700
                                                                                                                                                                                                                                                                                   Sequence 49, Application US/09266417; Patent No. 6228588; GENERAL INFORMATION:
                                                                                                                                                                             386 ATCATACTTTINCTCCTG 403
                                                                                                                                   2 ATCATGCTTTTTCTCCTG 19
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                                                Query Match 73.3%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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nucleic acid
DEDNESS: single
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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        US-09-265-315-49
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Pred. No. 1.9e+02;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: Storage
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 49, Application US/09265315
Patent No. 6187541
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                               386 ATCATACTTTINCTCCTG 403
                                                                                                                                                                                                                                                                                                       2 ATCATGCTTTTTCTCCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Martin, Patrick K. APPLICANT: Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 24 TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee, Ving J.
Malouin, Francois
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 49.
SEQUENCE CHARACTERISTICS:
LENGTH: 513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 49:
                                                                                                                                                                                                                   Ouery Match 73.3%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 513 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Benton, Bret
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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California
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STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
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Score 15.4; DB 4; Length 5631;
Pred. No. 2.4e+02;
0; Mismatches 1; Indels 0;
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                                 TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLILING LAILS. 14-APPLIL 1737
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9507766.5
FILING DATE: 13-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411900.5
FILING DATE: 14-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB94/02822
FILING DATE: 23-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326470.3
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/052,469 FILING DATE: Concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
                                                                                                                          Banner & Witcoff, Ltd
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: Concurrently hereverIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/08460751
                                                                                                                                              One Financial Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CATGCTTTTTCTCTGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 14-April-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPRANE: (617) 345-9100
TELEPRAN: (617) 345-9111
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5631 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.38;
94.18;
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ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Ke
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STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA
                                                                                NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner 6 V
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
Matches 16; Conserv
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CORIGINAL SOURCE:
                                                                                                                                                                    Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
FEATURE:
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CITY: B
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                                                                                                                                                                                          STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08969046B

Patent No. 6455762

GENERAL INCORMATION:
APPLICANT: Chiang, Vincent Lee C.
APPLICANT: Tsal, Chung-Jui
APPLICANT: Tsal, Chung-Jui
APPLICANT: Tsal, Chung-Jui
TILE OF INVENTION: Genetic engineering of trees through
TILE OF INVENTION: Genetic engineering of trees through
FILE REFERENCE: 881.003US1
CURRENT APPLICATION NUMBER: US/08/969,046B
CURRENT FILING DATE: 1997-11-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 1927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.4; DB 4;
Pred. No. 1.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15.4; DB 4;
Pred. No. 2.2e+02;
0; Mismatches 1
                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Lodes. Michael J.
APPLICANT: Mohamath, Roadoh
APPLICANT: Scriat, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIA
TITLE OF INVENTION: LUNG CANCER AND METHODS FOR T
FILE REFERENCE: 210121.475c1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT APPLICATION NUMBER: US 09/285,323
EARLIER FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 103
LENGTH: 741
                                                                                      US-09-370-838-103/c
; Sequence 103, Application US/09370838
Patent No. 6444425
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-09-052-469-1
'S Squence 1, Application US/09052469
'Patent No. 6380360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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        386 ATCATACTTTTNCTCCTG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 AGGCTTTTCTCCTGGG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Petroselinum crispum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CATCATGCTTTTTCTCC 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.3%;
ilarity 94.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 73.3%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: (64)...(1698)
US-08-969-046-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapien
US-09-370-838-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-08-969-046-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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NAME/KEY: misc_feature
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LOCATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 12912;
                                        APPLICANT: Reeders, Stephen
APPLICANT: Schoolder, Michael
APPLICANT: Schoolder, Michael
APPLICANT: Glucksmann, Sandra
TITLE OF INVENTION: IDENTICATION OF POLYCYSTIC KIDNEY
TITLE OF INVENTION: DISEASE GENE, DIAGNOSTICS AND TREATMENT
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-052-469-5
Sequence 5, Application US/09052469
Fatent No. 6380360
GENERAL INFORMATION:
APPLICANT: Harris et al.
TILLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
TITLE OF INVENTION: AND USES THEREOF
UNMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
STREET: ONE Financial Center
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-056/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,751
FILING DATE: 02-JUN-1995
ATTONNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/413,580
FILING DATE: 03-MAR-1995
ATTONNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 30,741
TELECOMMUNICATION NUMBER: 30,742
REFRENCE/DOCKET NUMBER: 30,742
REPRENCE/CHARACTERISTICS:
LEMOTH: 12912 base pairs
TWENTH: 12912 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.3%; Score 15.4; DB 2; 94.1%; Pred. No. 2.7e+02; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11031 CATGCTTTTTCTGCTGG 11047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 94.19
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
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ZIP: 02111
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1..12912
                                                                                                                                                                                                                                                                                STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
Patent No. 5891628
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-08-460-751-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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LOCATION: 1373..1701
OTHER INFORMATION: /function= "S3/S4 PETER fragment"
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LOCATION: 7295.8184
- OTHER INFORMATION: /function= "g alpha 22 fragment"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 6422.7294
OTHER INFORMATION: /function= "GAP GAMMA PETER
OTHER INFORMATION: fragment"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 2176..2962
LOCATION: 2176..2962
OTHER INFORMATION: /function= "S3/S4 CON2 PETER
OTHER INFORMATION: /function= "S3/S4 CON2 PETER
OTHER INFORMATION: /function= "S1/S3 PETER fragment"
OTHER INFORMATION: /function= "S1/S3 PETER fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /function= "S4/JH13 fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 3697.6421
OTHER INFORMATION: /function= "JH8 fragment"
MEDIUM TYPE: Floppy disk, 3.50 inch COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS . SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/052,469
FILING DATE: Concurrently herewith PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/422,582
FILING DATE: 14-APril-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08 9507766.5
FILING DATE: 13-APR-1995
PRIOR APPLICATION NUMBER: 08 9411900.5
FILING DATE: 14-JUN-1994
PRIOR APPLICATION NUMBER: 08 9411900.5
FILING DATE: 23-DEC-1994
PRIOR APPLICATION NUMBER: 33-56770.3
FILING DATE: 23-DEC-1994
PRIOR APPLICATION NUMBER: 33-993
ATPORNEY/AGRY INFORMATION:
NAME: Williams, Ph.D., Kathleen M. REGISTATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 34,380
REFERENCE/COCKET NUMBER: 34,380
REFERENCE (617) 345-9101
TELEPHONE: (617) 345-9101
TELEPHONE: (617) 345-9101
TELEFAX: (617) 345-9101
TELEFAX: (617) 345-9101
TYPE: NUCLEIC acid
STANDEDNESS: UNKNOWN
TTPER: NUMBER: MAKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
118..1372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANIEW
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Gaps
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                                                                              Length 14060;
                                                                                                                       1; Indels
                                                                                 Score 15.4; DB 3;
Pred. No. 2.7e+02;
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                                                                                                                                                                                                                                              Search completed: July 8, 2003, 09:32:17 Job time: 30.0402 secs
                                                                                                                                                                           11162 CATGCTTTTTCTGCTGG 11178
                                                                                                                                                          4 CARGCTTTTTCTCCTGG 20
                                                                                 Query Match 73.3%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                , NAME/KEY: CDS
; LOCATION: 135..13040
US-08-658-136-4
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                 Length 13807;
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                                                                                                                                                                                                 /function= "6 (5) R cDNA [Split]
fragment"
                                                                                                                                                                                                                                                                                        /product= "6 (5) R cDNA [Split]
fragment"
                        /function= "5' COMPLETE [Split]
fragment"
                                                                                                          /function= "5' COMPLETE [Split]
fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/POCKET WOMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANY: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: GENZYME CORPORATION ONE MOUNTAIN ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10900 CATGCTTTTTCTGCTGG 10916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08658136 Patent No. 6071717
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LOCATION: 87..117

OTHER INFORMATION: /produc

US-09-052-469-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 14060 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 1..85
OTHER INFORMATION: /funct
OTHER INFORMATION: fragmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature.
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Best Local Similarity 94.1<sup>§</sup>
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: ONE MOUNTAIN
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
                                                                                                LOCATION: 87.3696
OTHER INFORMATION:
OTHER INFORMATION:
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         LOCATION: 1..85
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-658-136-4
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Sequence 56, Sequence 56, Sequence 54,

Sequence 54, Appl Sequence 79, Appl Sequence 253, Appl Sequence 254, Appl Sequence 253, Appl Sequence 253, Appl Sequence 254, Appl Sequence 255, Appl

Sequence:

Title:

Run on:

Searched:

Database

2

Sequence 314, Sequence 204,

Sequence 2487, Sequence 7487, Sequence 1487, Sequence 6487,

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GENERAL INFORMATION:
Sequence 3, Application US/10095672A
Sequence 3, Application US/10095672A
Sequence 3, Application No. US20030068628A1
Sequence 3, Application No. US20030068628A1
Sequence 3, Application No. US2003006862BA1
SERVERAL INFORMATION:
APPLICANT: Tribel, Fredefic
TITLE OF INVENTION: NOLEDEOTIDE SEQUENCES CODING FOR VARIABLE RECIONS OF
TITLE OF INVENTION: PEPTIDE SEGMENTS AND THE DIAGNOSTIC AND THERAPEUTIC USES
FILE REFERENCE: 146.1185 CON-11.2-CON
TITLE OF INVENTION: PEPTIDE SEGMENTS AND THE DIAGNOSTIC AND THERAPEUTIC USES
FILE REFERENCE: 146.1186 CON-11.2-CON
CURRENT APPLICATION NUMBER: US 08/423,383
PRIOR PILLING DATE: 1992-10-23
PRIOR FILLING DATE: 1992-11-23
PRIOR FILLING DATE: 1992-11-23
PRIOR FILLING DATE: 1992-02-23
PRIOR PELLING DATE: 1992-02-23
PRIOR PELLING DATE: 1991-02-12
PRIOR PELLING DATE: 1991-02-12
PRIOR FILLING DATE: 1991-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 329
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                                                                                                                                                                                                                              US-09-884-441-253
US-09-884-441-254
US-09-884-975-648
US-09-983-965-5635
US-09-867-701-2945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 17.4; DB 9;
Pred. No. 1.2e+02;
0; Mismatches 1;
                                                       US-10-295-981-54

US-09-728-721-54

US-09-90-969-79

US-09-907-969-253

US-09-907-969-254

US-10-198-053-79

US-10-198-053-79

US-10-198-053-253

US-10-198-053-253
                                                                                                                                                                                                                                                                                                                                                                                        US-09-822-849A-204
IS-10-128-714-2487
                                                                                                                                                                                                                                                                                                                                                                       US-09-834-975-314
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; OTHER INFORMATION: IGR b 04; V BETA w23
US-10-095-672A-3
                       666666
                                                                                                                                        000000000
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q ID NO 3
LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 41, Appl
Sequence 70, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 152, Apl
Sequence 55, Appl
Sequence 55, Appl
Sequence 55, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Applisequence 124, Applesquence 124, Applequence 124, Applequence 11, Appl
                                                                                                                                (without alignments)
273.390 Million cell updates/sec,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                          July 8, 2003, 19:09:54; Search time 121.288 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US10_PUBCONB.seq:*/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCONB:seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCONB:seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpna/US06_PUBGOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBGOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO7_PUBGOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                               2210862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-918-995-24241

US-09-998-598-41

US-09-998-598-70

US-09-938-398-70

US-09-938-398-362

US-09-746-783-131

US-10-023-282-207

US-09-818-823-19

US-09-917-800A-1522

US-09-918-842A-3679
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US-10-125-540-124
US-09-764-870-124
US-09-864-921-11
                                                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                         1105431 seqs, 789497651 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_NA:*
                                                                        nucleic search, using sw model
                                                                                                                                                                                                                              21
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                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                           .US-09-647-780A-17
21
                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match ]
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82.9
82.9
80.0
80.0
80.0
80.0
778.1
777.1
777.1
76.2
76.2
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Maximum DB
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.4; DB 10;
Pred. No. 2.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.8; DB 9;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D
RECISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
SUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASLSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-918-995-24241.
; Sequence 24241, Application US/09918995; Publication No. US20030073623A1.
; GENERAL INFORMATION:
                                                                                                       US/09/263,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370711 TCATGCTTTGTCTCTGGG 370729
                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 CATCCTGCTTTGTCTCCTGG 404
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Patent No. US20020150922A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCATION: (1) ...(481)
COTHER INFORMATION: n = A,T,C or GUS-09-918-995-24241
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                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 82.9%;
Best Local Similarity 94.7%;
Matches 18; Conservative
Floppy disk
                                                                                                                      05-MAR-1999
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                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq, Inc.
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                                                                                                                             FILING DATE: 0
                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 24241
LENGTH: 481
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US-09-998-598-41
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Op
                                                                                                                                                                                                       APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
CORRESPONDENCES: 1279
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI NUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.4; DB 10; Length 1297;
Pred. No. 1.3e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25.
CURRENT APPLICATION DATA:
ELICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                  5: Seed and Berry LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   Sequence 288, Application US/09263959
Patent No. US20020150891A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  678 TCATGCTTTGTCTCGGG 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09263959
Patent No. US20020150891A1
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TCATGCTTTTTCTCCTGGG 21
                        TCATGCTTTGTCTCCTGGG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MOMSters, David D:
RECISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 1297 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.7
Matches 18; Conservative
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EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                      98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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ZIP: 98104-7092
                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CL'ASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
US-09-263-959-288
                                                                                                                                 US-09-263-959-288
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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AND METHODS FOR THE THERAPY AND
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Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16.8; DB 10; Length 1389;
Pred. No. 2.5e+02;
0; Mismatches 2; Indels 0:
                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/935,390A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Stolk, John A.

APPLICANT: The Chemanit, Ruth A.

APPLICANT: Meagher, Madelein Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corixa Invention Disclosure Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                  NAME: Jane E. R. Potter
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET.NUMBER: 1369.002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear : SEQUENCE DESCRIPTION: SEQ ID NO: 13: US-09-935-390A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/988,671
                                                                                                                                                                            FILING DATE: 22-Aug-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (510) 923-2718
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 362, Application US/09998598
Patent No. US20020150922A1
                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 131, Application US/09746783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        324 CATCCTGCTTTGTCTCCTGG: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CATCATGCTTTTTCTCCTGG 20
                                                                                                                                                                                                                                                                           FILING DATE: 1997-12-11 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 80.0%;
Best Local Similarity 90.0%;
Matches 18; Conservative
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I Similarity 90:0%;
18; Conservative
                           COMPUTER READABLE FORM
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SEQ ID NO 362
LENGTH: 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-998-598-362
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Best Local Si
Matches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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APPLICANT: Chenault, Ruth A.
APPLICANT: Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
TILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: CORIXA INVENTION DISClosure Database
                APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.561
CURRENY APPLICATION NUMBER: US/09/998,598
CURRENY FILING.DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SEQ ID NO 41
LENGTH: 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 566;
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Pred. No. 2.3e+02;
0; Mismatches 2;
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Williams, Lewis T.
Kothakota, Srinivas
TITLE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                     80.0%; Score 16.8; D
90.0%; Pred: No. 2.3e
iive 0; Mismatches
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Patent No. US20020076761A1
GENERAL INFORMATION:
APPLICANT: Escobedo, Jalme
Oulanjin, Hu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 CATCTGCTTTGTCTCTGG 253
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Best Local Similarity 90.0%;
Matches 18; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                          , TYPE: DNA
, ORGANISM: Homo sapiens
US-09-998-598-41
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ORGANISM: Homo sapiens
US-09-998-598-70
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Best Local Similarity
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APPLICANT:
APPLICANT:
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER APPLICATION NUMBER: 60/048,963
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* APPLICATION NUMBER: 60/048,917

* APPLICATION NUMBER: 60/048,949

* FILING DATE: 1997-06-06

* APPLICATION NUMBER: 60/048,949

* FILING DATE: 1997-06-06

* PRILING: DATE: 1997-06-08

* PRILING: DATE: 1997-06-08

* APPLICATION NUMBER: 60/048,883
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LICATION NUMBER: 60/048,970
ING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,876
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PLICATION NUMBER: 60/048,899
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PLICATION NUMBER: 60/048,900
LING DATE: 1997-06-06
PLICATION NUMBER: 60/048,901
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PLICATION NUMBER: 60/048,915
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LICATION NUMBER: 60/048,972
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PLICATION NUMBER: 60/048,916
LING DATE: 1997-06-06
PLICATION NUMBER: 60/049,373
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APPLICATION UNMBER: 60/048,877
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,878
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PPLICATION NUMBER: 60/070,923
ILING DATE: 1997-12-18
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PPLICATION NUMBER: 60/048,884
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PPLICATION NUMBER: 60/048,894
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PLICATION NUMBER: 60/048,892
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PPLICATION NUMBER: 60/049,374
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                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.8; DB 9; Length 1425; Pred. No. 2.5e+02; 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/746,783
FILING DATE: 2.1-Dec-2000
CLASSIFICATION: <a href="https://doi.org/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/10.1007/
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SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-746-783-131
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/10/023,282
CURRENT FILING DATE: 2001-12-20
EARLIER APPLICATION NUMBER: 09/205,258
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER APPLICATION NUMBER: PCT/US98/11422
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/048,885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/049,375
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NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION:
                                                                                                                                                            Racie, Lisa A.
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael J.
Howes, Steven H.
Fechtel, Kim
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Publication No. US20030092893A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 227-7400
TELEFAX: (617) .742-4214
Publication No. US20030044935A1
GENERAL INPORMATION:
APPLICANT: Jacobs, Renneth
MCCOy, JOHN M.
LAVAllie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATCCTGCTTTGTCTCCTGG 337
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LENGTH: 1425 base pairs
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STRANDEDNESS: single
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Best Local Similarity 90.0%;
Matches 18; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cambridge
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US-10-023-282-207
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; OTHER INFORMATION: Genbank Accession No. US20020119462A1 X98517 US-09-917-800A-1522
                                                                 PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR PILING DATE: 2001-05-15
PRIOR PELICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR FILING DATE: 2001-05-06-06
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR PILING DATE: 2001-06-13
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/303,459° PRIOR FILING DATE: 2001-07-09
                           ILING DATE: 2000-11-02 PPLICATION NUMBER: US 60/290,029
    APPLICATION NUMBER: US 60/222,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CATGCTTTTTTCTCGGG 21
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ilarity 94.4%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1522
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           PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Wethod for the Treatment and Prevention of Dental Caries FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR PPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 482;
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Pred. No. 2.5e+02;
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Pred: No. 3.5e+02;
0; Mismatches 1
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EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 207
LENGTH: 1480
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Patent No. US20020119462A1
                                                                                                                                                                                                                                                                                                                                                               379 CATCCTGCTTTGTCTCTGG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09881823
Patent No. US20020068066A1
                                                                                                                                                                                                                                                                                                                     1 CATCATGCTTTTTCTCCTGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 TCATGCTCTTTCTCTGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANDERSON, MAXWELL
MORRISON, SHERIE
TRINH, RYAN
WIMS, LETITIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 78.1%;
Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                          Match 80.0%;
Local Similarity 90.0%;
es 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Elashoff, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene Logic, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mendrick, Donna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castle, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHI, WENYUAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson, Kory
                                                                                                                                                         ORGANISM: Homo sapiens US-10-023-282-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (27)..(482)
US-09-881-823-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-881-823-19
                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sednence .19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 19
                                                                                                                                                                                                                             Query Match
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Gaps

Indels

Score 16.4; DB 10; Length 1632; Pred. No. 3.9e+02; 0; Mismatches 1; Indels 0;

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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE. OF INVENTION: SAME, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.4; DB 9; Length 2000;
Pred. No. 4e+02;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US.60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3679
LENGTH: 2000
                                                                                                                   Sequence 3679, Application US/09938842A. Patent No. US20020160378A1. GENERAL INFORMATION:
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579 CATGCTTTTTATCCTGGG 596
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Best Local Similarity 94.4%
Matches 17; Conservative
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US-09-778-844-54/C
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; OTHER INFORMATION: Description of Unknown Organism: EMBL No. US20020150971A1 q9ulg1
US-09-778-844-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Unknown Organism: EMBL No. US20020150971A1 q9ulg1
US-09-778-844-55
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APPLICANT: SCHALLING, MARTIN
TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES FOR CONTROLLING FOOD
TITLE OF INVENTION: INTAKE AND/OR BODY WEIGHT
FILE REFERENCE: 030307/0195
CURRENT APPLICATION NUMBER: US/09/778,844
CURRENT APPLICATION NUMBER: US/09/778,844
SOFTWARE: PATENTIN VET. 2.1
                                                                                                APPLICANT: SCHALLING, MARTIN
TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES FOR CONTROLLING FOOD
TITLE OF INVENTION: INTAKE AND/OR BODY WEIGHT
FILE REFERENCE: 030307/0195
CURRENT APPLICATION NUMBER: US/09/778,844
CURRENT APPLICATION NUMBER: US/09/778,844
SUBBER OF SEQ ID NOS: 206
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.2; DB 10;
Pred. No. 4.6e+02;
0; Mismatches 3;
                                                    GENERAL INFORMATION:
APPLICANT: JOHANSEN; JEANETTE ELISABETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 CATCTTCCTTTTCTTCGG 496
Sequence 54, Application US/09778844 Patent No. US20020150971A1
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Best Local Similarity 85.7%;
Matches 18; Conservative
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ORGANISM: Unknown Organism
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ORGANISM: Unknown Organism
FEATURE:
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LENGTH: 1160
                                                                                                                                                                                                                                                                                                       SEQ ID NO 54
LENGTH: 1156
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Indels

Search completed: July 9, 2003, 02:22:32 Job time : 123.338 secs

1 CATCATGCTTTTTCTCCTGGG 21

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C 7 18 85.7 378 9 AJ489153 AJ489154 AJ4	Fax: b25 286 235/ Email: gwaldbleser@ars.usda.gov Single pass sequencing. Bases called with Phred v0.000925.c. Low quality bases and vector trimmed with Lucy v1.16. Plate: Br1_6 row: B column: 10
	 -
GenCore version 5.1.6	. 5 39 10 1872268 AN921249 .7 291 13 B1435848 B1435848 .7 331 14 BQ120752 BM108635

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of the following tissues: thalamus, cerebellum,
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Best Local Similarity
Matches 19; Conserv
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ORIGIN
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ORIGIN
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KEYWORDS
SOURCE
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AI872268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized medulla library CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                               /db_xref="taxon.7998"
/clone="IpcGBr1_6_B10_21_15Feb00_077"
/clone_llb="Ictalurus punctatus Brain1 primary library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 Eckstein Medical Research Building Iowa City, IA 52242, USA el: 319 335 8250 - ax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW521249
UI-R-BOO-agk-h-12-0-UI.sl UI-R-BOO Rattus norvegicus cDNA clone
UI-R-BOO-agk-h-12-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     /note="Organ: brain; Vector: pSportl; .Site_1: Sal 1; Site_2: Not 1; Primary library" 52 c 81 g 42 t
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                                                                                                                                                                                                                                                                                                                           Length 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ontact: Soares, MB rogram for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                       Score 18.4; DB 13;
Pred. No. 7.8e+02;
); Mismatches 1;
                                                           organism="Ictalurus punctatus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="UI-R-B00-agk-h-12-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Senome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Sprague-Dawley
                                                                                                                                                              /sex="female and male"
/dev_stage="adult"
/lab_host="DH10B"
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                       Location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                136 CATCATGCTTTTCTCCTTG 117.
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Seg primer: M13 Forward
POLYA=Yes.
                                                                                /strain="USDA103
                                                                                                                                                                                                                                                                                                                                                                                                           1 CATCATGCTTTTTCTCCTGG 20
Seq primer: M13 Reverse
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                                                                                                                                                                                                                                                                                                                         87.6%;
95.0%;
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                                                                                                                                                                                                                                                                                                                                                                   19; Conservative
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Matches 19; Conserv
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AUTHORS
TITLE
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MEDLINE
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AW521249
LOCUS
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SOURCE
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tz62h02.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293203 3' similar to contains Alu repetitive element;, mRNA sequence.
AI872268.1 GI:5546317
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                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                    derived, please visit our web site at ratest.eng.ulowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 397) NCI-GAAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; This library represents the normalized version of NCI_GAP_0v23. Cloned unidirectionally. Primer: Oligo dr. Average insert size 0.86 kb. Tumor types include: mixed Mullerlan tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Constructed by Life Technologies.
     cortex,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
hypothalamus, medulla, pons, midbrain, cerebral corte corpus striatum and hippocampus. For a detailed description of the library from which this clone was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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/tissue_type="tumor, 5 pooled (see description)"
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                                                                                                                                                                                                                                                                                                                                                                         Score 18.4; DB 10;
Pred. No. 9e+02;
0; Mismatches 1;
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Insert Length: 1416 Std Error: 0.00
Seg primer: -400P from Gibco.
Location/Qualifiers
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Best Local Similarity 95.0%;
Matches 19; Conservative
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Unpublished (1997)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Matches 18; Conserv
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EST538609 P. infestans-challenged leaf Solanum tuberosum cDNA clone
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                                                                                                                                                                                                                                                                                                                                                Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B. Generation of ESTs from Potato Leaves Challenged with Phytophthora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote—Wordor: Bluescript SK(-); Site_1: EcoRI; Site_2: Khol: Whole plants were challenged with 450,000 sporangia/ml P. infestans US-1(08 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 17-APR-2002
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicofyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, I
Division tel 1-800-711-6195, email cdna@resgen.com
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/Lissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
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100.0%; Pred. No. 1.2e+03;
11ve 0; Mismatches 0;
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/db_xref="taxon:4113"
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EST556171 potato roots Solanum tuberosum cDNA clone cPRO1H16 5' end 'mRNA sequence.

BM108635
BM108635.1 GI:17069013
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/tissue_type="mixed tissues"
/tab_host="sour"
/note="vector: pBluescript SK(-); Site_l: EcoRI; Site_2:
XhoI; supplier: Combination of untreated and Phytophthora infestans treated libraries of stolons, leaves, leaflets,
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
I (bases 1 to 31)
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Garamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
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9712 Medical Center Dr. Rockville, MD 20850, USA
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/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: potato@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robin Buell
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Wed Jul

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/tissue_type="roots"
                                                                                                                                                                                                                                                                                                            Cocation/Qualifiers
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Best Local Similarity 100.0%; Pr
Matches 18; Conservative 0;
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GI:18259259
                                                                                                                                                                                                                                           Email: cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           African clawed frog.
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                                 potato.
Solanum tuberosum
                                                                                                                                                                                                                                                                                           Seq primer: T3.
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 BM407629.1
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BG019241/c
LOCUS
DEFINITION
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ORIGIN
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JOURNAL
COMMENT
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VERSION
KEYWORDS
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AUTHORS
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KEYWORDS
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                                                                             /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Abol; Shol; supplier: Cornell Onlersalty, Tanksley lab; sequencing; The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium.
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1 (bases 1 to 378)
Gebhardt,C., Walkemeier,B., Henselewski,H., Barakat,A., Delseny,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparative mapping between potato (Solanum tuberosum) and Arabidopsis thaliana reveals structurally conserved domains and ancient duplications in the potato genome Unpublished (2002) Contact: Gebhardt Contact: Gebhardt
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                                                                                                                                                                                                                            Score 18; DB 13; Length 336;
Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="S3b7"
/clone_lib="Solanum tuberosum cv. Saturna"
57 c 95 g 67 t
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                                 /tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
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MPI for Breeding Research
Carl-von Linne Weg 10, Cologne, D-50829,
Location/Qualifiers
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/db_xref-"taxon:4113"
                                                                                                                                                                                                                85.7%; Sco.
100.0%; Pre
0;
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Similarity 100.0%; P
18; Conservative 0;
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AJ489153
                                                                                                                                                                                                                                                              Conservative
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BM407629
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Best Local Similarity
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Best Local Similarity
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ORIGIN
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BM407629/c
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AUTHORS
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KEYWORDS
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1 (bases 1 to 463)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylle,T., Underwood,K., Theising,B., Bowers,Y., Person
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Washu and Wilson,R.
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Mote_isupplier: Corneal University, Tanksley lab; sequencing; The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."
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INAGE:4061625 5' similar to SW:N4AN_HUMAN 095182 NADH-UBIQUINONE
OXIDOREDUCTASE SUBUNIT B14.5A ;, mRNA sequence.
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Subardium. Locatosum. Straptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Steridae; euasterida; Is Solanales; Solanaceae; Solanum.

( pases 1 to 416)

Utterpack, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tankaley, S. and Baker, B.

Generation of ESTS from potato roots
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Washlu Xenopus EST project, 199
Washlugton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                 For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 416;
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/lab_host="SOLR"
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                                                                                                                                                                                                                                                                               Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
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Pred. No. 1.4e+03; 7; Mismatches 0;
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/organism="Solanum tuberosum"
/cultivar="Kennebec"
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/clone="cPR031D6"
/clone_lib="potato roots"
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Best Local Similarity
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                                                                                                                                Query Match
                                                                     BASE COUNT
ORIGIN
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BG890211/c
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BM405275/c
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ORIGIN
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                                                                               Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@lmage.llnl.gov Seq primer: -40RP from Gibco High quality sequence stop: 400.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM109913 504 bp mRNA linear EST 26-NOV-2001
EST557449 potato roots Solanum tuberosum cDNA clone cPRO5N21 5' end
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                                                                                                                                                                                                                                                                                                                                                                                                                       (Department of Developmental and Cell Biology, University of California, Irvine).
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(bases 1 to 504)
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Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,
Tanksley,S. and Baker,B.
                          Library constructed by C. Hashimoto, Ph.D: in the laboratory of Cho, Ph.D: DNA Sequencing by: Washington University Genome Sequencing Center
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(hoI; supplier: Cornell University, Tanksley lab.
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For clone info: please contact Research Genetics,
Division tel 1-800-711-6195, email cdna@resgen.com
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/lab_host="SOLR"
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                                                                                                                                                                                                 /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:4061655"
/clone_lib="Cho Li treated gastrula"
/fissue_type="gastrula, Li-treated"
/lab_host="DH10B"
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Pred. No. 1.4e+03;
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'clone="cPRO5N21"
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Best Local Similarity
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BM109913/c
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                        CM medium
                   isolated from in vitro grown stem cuttings on CM medi
Roots were isolated two weeks after placing the stem
cuttings from in vitro grown plants on medium."
73 c 120 g 105 t
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Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 504)
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The Institute for Genomic Research.
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                                                                                                                                                               Length 504;
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/lab_host="SOLR"
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Pred. No. 1.5e+03;
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Generation of ESTs from potato roots
Unpublished (2001)
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/clone="cPRO23K18"
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100.0%; Pred
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100.0%; Pre
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BM405275
BM405275.1 GI:18256785
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Tel: 1-800-711-6195
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Matches 18; Conservative
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/db_xref="taxon:4113"
/clone="cPRO29E20"
/clone_lib="potato roots"
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                                                                                    /db_xref="taxon:4113"
/clone="cPRO30J14"
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Best Local Similarity 100.0%; P
Matches 18; Conservative 0;
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Solanum tuberosum
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Seq primer: T3
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EST581746 potato roots Solanum tuberosum cDNA clone cPRO30J14 5'
EM407419
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XhoI; This library targets genes expressed in dormant
tubers. This library was made from sections of dormant
tuber, avoiding the buds and epidermis. Tubers were stored
for one month post-harvest at 4cc. The tuber was peeled,
well away from the surface. Then it was chopped into 1-2
mm cubes and immediately frozen in liquid nitrogen. This
library is noted as 94 in Tanksley lab notebooks."
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                                                                                        Solation tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 518)
van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chiemingo,A.,
Bengri,O., Buell,C.R., Fooning,C., Tanksley,S. and Baker,B.
Unpublished (2001)
The Institute for Genomic Research
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Utterback,T., Chiemingo;A., Bougri,O., Buell,C.R., Ronning,C.,
Tanksley,S. and Baker,B.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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For clone info: please contact Research Genetics, 1
Division tel 1-800-711-6195, email cdna@resgen.com
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Division tel 1-800-711-6195, email cdna@resgen.com
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/dev_stage="one month post-harvest"
/lab_host="SOLR"
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Pred. No. 1.5e+03;
0; Mismatches 0;

    518
    forganism="Solanum tuberosum"
/cultivar="Kennebec"

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/clone="cSTD17H15"
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Matches 18; Conserv
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EST581264 potato roots Solanum tuberosum cDNA clone CPR029E20 5' end, mRNA sequence.

BM406937.1 GI:18258567
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cuttings from in vitro grown plants on medium."
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wan der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,
Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.,
Tanksley, S. and Baker, B.
Generation of ESTs from potato roots
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/lab host="SOLR"
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/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; L
1.5e+03;
/organism="Solanum tuberosum"
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/organism="Solanum tuberosum"
/cultivar="Kennebec"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18; DB 1
Pred. No. 1.5e
0; Mismatches
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us-09-647-780a-17.rst

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EST582168 potato roots Solanum tuberosum cDNA clone cPRO32M20 5' mina sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Shol; supplier: Cornell University, Tanksley lab; Sequencing; The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium.
                                                                                                                                                                                                                                                                                                                                                                         Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 537)
van der Hooven,R., Sun,H., Karamycheva,S.A., Tsai,J., Van Aken,S.,
Utterback,T., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.,
Tanksley,S. and Baker,B.
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                 ö
        Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match

85.7%; Score 18; DB 13; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'tissue_type="roots"
'dev_stage="in vitro grown stem cuttings"
'lab_host="SOLR"
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
Contact: Research Genetics, Libraries Division
      DB 13; L
1.5e+03;
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/cultivar="Kennebec"
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ch 85.7%; Score 18; DB 1 Similarity 100.0%; Pred. No. 1.5 18; Conservative 0; Mismatches
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clone="cPRO32M20"
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                                                                                                      272 CATCATGCTTTTCTCCT 255
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8, 2003, 09:22:04

Search completed: July Job time: 1068.8 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ranslation="MGKSESSVGMMERADNCGRRRLGFVECGLLVLLTLLLMGAIVTL
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nep ii membrane metalloprotease and its use for screening inhibitors useful in therapy Patent: WO 9953077-A 1 21-0CT-1999; INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); GUIMET TANIA (FR); ROSE CHRISTIANE (FR); BONHOWME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
Location/Qualifiers
Patent: WO 9953077-A 18 21-OCT-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS
CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME
MARIE CHANTAL (FR); FACCHIMETTI PATRICIA (FR)
Location/Qualifiers
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735 c 787 g 559 t
                                                                                                                                                                                                              Score 21; DB 6;
Pred. No. 1.1;
Mismatches 0

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    /organism="synthetic construct"
    /db_xref="taxon:32630"

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Schwartz,J.C., Gros,C., Ouimet,T.,
Facchinetti,P.
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Sequence 1 from Patent W09953077.
AX014701
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Mammalia; Eutheria; Rodentia;
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Adams, C., Add.-Oduola, B., Alt-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Babrooks, S.L., Amaratunge, H.C., Are, J.R., Bonnin, D., Bauck, J., Bowie, S. Brieva, M. Brown, E., Brown, M. Bryant, N.P., Bulay, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathonne, S.R., David, R., Davila, M.L., Davis, C., Dany, T., Daderich, D.A., Delaney, K.R., Delando, O., Den, Y.L., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Roster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunartne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Gallins, B., Homsi, F., Howard, S., Huber, J., Hull, S., Hume, J., Jackson, E., Jackson, R., Jaly, Y., Johnson, R., Molloway, C., Lewis, L., Li, J., Li, Z., Licharge, C., Lieu, C., Lieu, G., Lieu, C., Liewis, L., Li, J., Li, Z., Licharge, C., Martindale, A., Martindale, R., Mar
ACO94732 174953 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus clone CH230-516, *** SEQUENCING IN PROGRESS ***,
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------- Project Information
Center project name: GBGF
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                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is subtirary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                       Consensus quality: 152255 bases at least Q40
Consensus quality: 158448 bases at least Q30
Consensus quality: 164461 bases at least Q20
Estimated insert size: 155965; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
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Shirotani, K. and Saido, T.C.
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Shirotani, K. and Saido, T.C.
Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Institutte, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
351-0198, Japan
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Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 rapidity and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
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Mus musculus soluble secreted endopeptidase delta mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'product="neprilysin-like peptidase alpha"
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Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                Mammalia; Eutheria; Rodentia;
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AF157106.1 GI:6467400
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watches 20; Conservative
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AF157106/c
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NNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLN
FGGIGMVIGHEITHGFDDNGRNFDKNGNMLDMWSNFSARHFQQOSQCMIYQYGNFSWE
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AQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPWKRCR
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DIIRDELEVILKGVLEDSTSQHRPAVEKAKTIYRSCMNQSVIEKRDSEPLLSVLKMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SEP(delta); metalloprotease; alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIALRD
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Molecular identification and characterization of novel mambrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a variety of vascactive peptides J. Biol. Chem. 274 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (08-JUN-1999) International Center for Medical Research,
Robe University School of Medicine, 7-5-1 Kusunoki, Chuo, Robe
6500017, Japan
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Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T., Iwatsubo, T. and Saido, T.C.
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Mus musculus neprilysin-like peptidase beta mRNA, complete cds
AF302076
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J. Biol. Chem. 276 (24); 21895-21901 (2001)
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Pred. No. 11;
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db_xref="G1:6467401"
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Ikeda,K., Emoto,N. and Matsuo,M.
Direct Submission
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Direct Submission
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AF157105/c
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FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYRAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
                                                                                                                                                                                                                                                                             /translation="MVERAGWCRKKSPGFVEYGLAVLLLLLLGAIVTLGVPYSIGKQL
PLLTSLLHFSWDERTVVKRALRDSSLKSDICTTPSCVIAAARILENADQSRNPCENFY
                                                                                                                                                                                                                                                                                                                     QYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRS
                                                                                                                                                                                                                                                                                                                                        CMNQSVIEKRDSEPLLSVLKMVGGWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVL
                                                                                                                                                                                                                                                                                                                                                            IDLF IWNDDQNSSRHVIY I DQPTLGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRK
                                                                                                                                                                                                                                                                                                                                                                            DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQERFGLKG
                                                                                                                                                                                                                                                                                                                                                                                                 FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
                                                                                                                                                                                                                                                                                                                                                                                                                   RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
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                            lc Neuroscience Laboratory, Brain
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Maruyama, K., Tabubuki, S., Iwata, N., Takaki, Y., Harigaya, W., Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T., Iwatsubo, T. and Saido, T.C.
Iwatsubo, T. and Saido, T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thioppan and phosphoramidon-sensitive endopeptidases
J. Blol. Chem. 276 (24), 21895-21901 (2001)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory
Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saltama
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                                                                                                                                                                                                                        'product="neprilysin-like peptidase beta"
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0; Mismatches
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                                                                                                                    /organism-"Mus musculus"
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/db_xref="taxon:10090"
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                                                                                                                                                                                 /note-"endopeptidase"
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/note="endopeptidase"
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Direct Submission
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AF157105 2892 bp mRNA linear ROD 25-NOV-1999
Mus musculus soluble secreted endopeptidase mRNA, complete cds.
AF157105
                                                                                                                              LGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLEIET
HLANATVPQEKRHDVTALYHRMDLMELQERFGLKDRVSLCSPGCPGTHSVDQAGLELG
                                                                                                                                                                                                                                                                                                                         GAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMVIGHEITHGFDDNGR
                                                                                                                                                                                                                                                                                                                                                    NFDKNGNMLDWWSNFSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNG
                              SSLKSDICTTPSCVIAAARILENMOQSRNPCENFYQYACGGWLRHHVIPETNSRYSNF
DILRDELEVILKGVLEDSTSQHRPAVEKAKTLYRSCMNQSVIEKRDSEPLLSVLKMYG
                                                                                             GWPVAMDKWNETMGLKWELERQLAVLNSQFNRRVLIDLFIWNDDQNSSRHVIYIDQPT
                                                                                                                                                                                          NPPASDSRVLGLKGFNWTLF1QNVLSSVEVELFPDEEVVVYG1PYLENLED11DSYSA
                                                                                                                                                                                                                        RTMQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESA
                                                                                                                                                                                                                                                          VGSLYIKRAFSKDSKSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQI
                                                                                                                                                                                                                                                                                    GYPDYILEDNNKHLDEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWII
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DQNLSKESAMVREEMAEVLELETHLANATVFQEKRHDVTALYHRMDLMELQERFGLKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular identification and characterization of novel membrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a variety of vasoactive peptides J. Blol. Chem. 274 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2892)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Yokoyama,M. and Matsuo,M.
/translation="MVERAGWCRKKSPGFVEYGLMVLLLLLLGAIVT
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Pred. No. 11;
0; Mismatches
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eda,K., Emoto,N. and Matsuo,M.
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/organism="Mus
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ilarity 95.2%;
Conservative
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ROD 11-MAY-2000

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Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                      Ghadar,G., Ruchon,A.F., Carpentier,M., Marcinkiewicz,M., Seidah,N.G., Crine,P., Desgroseillers,L. and Boileau,G. Molecular choning and blochemical characterization of a new mctestis soluble-zinc-metallopeptidase of the neprilysin family Biochem. J. 347 (Pt 2), 419-429 (2000)
2925 bp mRNA linear ROD 11.
neprilysin-like metallopeptidase 1 (N11) mRNA.
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Pred. No. 11;
0; Mismatches
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797 c 836 g 582
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/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="testis"
1. 2925
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/db_xref="G1:7769083"
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Rođentia;
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ilarity 95.2%;
Conservative (
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/gene="N11"
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Mammalia; Eutheria; F
1 (bases 1 to 2925)
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Bolleau, G. and Desgroseillers, L.
New metalloproteases of the neprilysin family
Patent: WO 0047750-A 12 17-AUG-2000;
BOILEAU GUY (CA); DESGROSEILLERS LUC (CA); UNIVERSTIE DE MONTREAL
                                                           OIVEPAGILQPPFESKDOPQSLNFGGIGMVIGHEITHGFDDNGRNFDKNGNMLDWWSN
FSARHFQQGSQCMIYQYGNFSWELADNQNVNGFSSLGENIADNGGYRQAYKAYLRWLA
DGGRDQRLDRLTYAQLFFINYAQVWGGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
LDGFSEBAFHCPRGSPWHPMKRCHIW"
774 c 827 g 574 t
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DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
       RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
KSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
DEEYSSLTFYEDLYFENGLQNLKNNAQRSLKKLREKVDQNLWIIGAAVVNAFYSPNRN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 11;
); Mismatches 1;
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'note="unnamed protein product"
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Pred. No. 11;
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Sequence 12 from Patent WO0047750.
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/db_xref="taxon:10090".
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llarity 95.2%;
Conservative
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Best Local Similarity 95.2%;
Matches 20; Conservative
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Matches 20; Conserv
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AX033272/c
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AF176569/c
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AUTHORS
TITLE
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FEATURES

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Mus musculus clone RP24-553K14, LOW-PASS SEQUENCE SAMPLING.
AC120432
AC120432.1 GI:20455766
HTG; HTGS, PHASEO.
Mus musculus
Ruberner.
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RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
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DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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IDLFIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKVRRAYLEFMTSVATMLRK
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2 (bases 1 to 2925)
Ghaddar,G., Ruchon,A.F., DesGroseillers,L. and Boileau,G.
Direct Submission
Submitted (09-AUG-1999) Biochemistry, University of Montreal, 2900
Edouard Montpellt, Montreal, Que H3T 1J4, Canada
Location/Qualifiers
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132 9531: 340 of 100 bp 732 9731: 349 of 10448: contig of 717 bp in length 1449 10548: gap of 100 bp 11268: contig of 720 bp in length 1269 1368: gap of 100 bp in length 1369 12087: contig of 749 bp in length 1293: contig of 744 bp in length 1293: 13031: gap of 100 bp in length 1293: contig of 744 bp in length 13932 13031: gap of 100 bp in length 13932 13031: gap of 100 bp in length 13932 13031: gap of 100 bp in length 13932 13880: gap of 100 bp
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17836: contig of 683 bp in length
36: gap of 100 bp
18651: contig of 715 bp in length
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   Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                              Gardyna, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Genome
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                                                                                                                                                                                                                                                               M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
                                                                                                                                                       DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S. P., FitzHugh, W., Gage, D., Galagan, J., Gardynk Goyette, M., Graham, L., Grand-Pierre, N., Hulme, W., Illev, I., Johnson, R., Jones, C.,
                                                                                                                                                                                                                                                                                                                                                                           n.A., Talamas,J., Tesfaye,S., Theodore,
Travis,N., Trigilio,J., Vassiliev,H.,
B., Wu,X., Wyman,D., Ye,W.J., Young,G.
                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N
Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L.,
                                                                                                                                                                                                                      LaRocque,K., Lamazares,R.,
R., Lindblad-Toh,K., Liu,G.,
J., Marquis,N., Matthews,C.
                                                                                                                                                                                                                                                                                                                                    ., Rogov, P
                                                                                                                                                                                                                                                                                                                 Phunkhang, P., Pierre, N., Pollara, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-MAY-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                       Bastien, V., Bloom, T., Bogusla
L., Camarata, J., Campoplano, A.
Colangelo, M., Collins, S., CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        However, it should not be assumed that this clone
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                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-553K14
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, Lehoczky,J., Levine,R
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                                                                                                                                                                                                                                                                                                                                            , Rosetti, M
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                                                                                                                                                       Cooke, P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved;
                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                           Viel, R.,
            REFERENCE
AUTHORS
TITLE
                                                          JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
```

COMMENT

```
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 25, 2002 this sequence version replaced gi:21627906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                             Insert size: 208149; sum-of-contigs
Insert size: 219051; 2.3% error; agarose-fp
Quality coverage: 12.41x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS TBBCHR1A Accession AL359782
                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown
                                                                                                                                                                                                                                                                                                                                                                                                                    the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 208249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137304 137403: gap of 100 bp
137404 208249: contig of 70846 bp in length.
Location/Qualifiers
                                                                                                                                                     Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                               Chemistry: Dye-terminator Big Dye; 88% of reads Consensus quality: 20784 bases at least Q40 Consensus quality: 207956 bases at least Q30 consensus quality: 208060 bases at least Q20
                                                                                                                                                                                                                                                                                                           coverage: 12.08x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note-"assembly_fragment:04071"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137404. .208249
/note="assembly_fragment:01838
                                            Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
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53647 c 51328 g 49076 t
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                                                                                                                                                                                                                                                                                                                                                                                                                    This record will be updated with
                                                                                          Contact: humquery@sanger.ac.uk
                                                                            Web site: http://www.sanger.ac.uk
                                                                                                                                       Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism-"Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="taxon:10090'
'chromosome="4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="RP23-15L19"
/clone_lib="RPCI-23"
                                 -- Genome Center
                                                                                                                         Center project name: bM15L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          810000
                                                                                                                                                                                     Themistry: Dye-terminator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence split into 10 fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_end:T7
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800001
900001
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Matches 20; Conserv
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TBBCHR1A_00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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TBBCHRIA_02
TBBCHRIA_03
TBBCHRIA_04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TBBCHR1A_05
TBBCHR1A_06
TBBCHR1A_07
TBBCHR1A_08
TBBCHR1A_09
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                 COMMENT
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Mus musculus chromosome 4 clone RP23-15L19, *** SEQUENCING IN
PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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744 bp in length
100 bp
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                                                                                                                                         100 bp
706 bp in length
                                                                                                                                                                     o of 100 bp contig of 712 bp in length of 0 bp
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49 bp in length
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contig of 694 bp in length
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                                              100 bp of 740 bp in length
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732 bp in length
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721 bp in length
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of 732 bp
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Pred. No. 13;
0; Mismatches
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98: contig of
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Mammalia; Eutheria; Rodentia;
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54832; con+
                                         40038: cont
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ilarity 95.2%;
Conservative
            38460: gar
39198:
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Best Local
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AL607032/c
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VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
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q

Gaps

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Plowman, G.D., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and
                                                                                                                                                                                                                                Length 2232;
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                                                                                                                                                                                                                              DB 6;
                                             Novel proteases
Patent: WO 0183782-A 28 08-NOV-2001;
                                                                                                                                                                                                                            k; Score 17.8; I
k; Pred. No. 89;
0; Mismatches
                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
a 620 c 705 g 39
                                                                                                                                                                                                                                                                                                                                                                                        8, 2003, 03:35:06
                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                1 CCCGAAGTTTCTTGAGGCTCC 21
                                                                                                                                                                                                                            84.8%;
                                                                                                                                                                                                                                                           19; Conservative
                                                                                  Sugen, Inc. (US)
                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                    Search completed: July Job time: 234.102 secs
                             Payne, V
                                                                                                                     source
                                                                                                                                                                     BASE COUNT
ORIGIN
            AUTHORS.
                                                            JOURNAL
                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                 qq
Continuation (7 of 10) of TBBCHRIA from base 600001 (AL359782 Trypanosoma brucei chromos
                                                                                                                                                                                                                                       PAT 08-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNYSWDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWMAEGGKDQQLPGLDLTHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILEVVGGWPVAMDRWNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNSSRH:
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                        DB 2; Length 110000;
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                                                                         Indels
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Deleershijder,W., Wiegers,R. and Weske,M.
Human enzymes of the metalloprotease family
Patent: WO 0136610-A 1 25-WAY-2001,
Solvay Pharmaceuticals B.V. (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match (84.8%; Score 17.8; DB 6; Best Local Similarity 90.5%; Pred. No. 89; Matches 19; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="unnamed protein product"
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                                    Score 18.4; DB
Pred. No. 49;
0; Mismatches
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                                                                                                                                                                                                                              Sequence 1 from Patent W00136610.
AX146976
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                            Location/Qualifiers
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                                    Query Match 87.6%;
Best Local Similarity 95.0%;
Matches 19; Conservative
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S. pneumoniae SP05
M. capsulatus gene
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DNA encoding a mou-
DNA encoding mouse
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Human neprilysin-1
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Human protease, PR
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                                                                                                                                        Human
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AAH31170
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AAC42424
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Schwartz JC;
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Rat membrane metal
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358.431 Million cell updates/sec
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/SIDS2/gcgdata/geneseqr.emb1.NA1991.DAT:
/SIDS2/gcgdata/geneseqr.emb1.NA1991.DAT:
/SIDS2/gcgdata/geneseqr.emb1.NA1991.DAT:
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/SIDS2/gcgdata/geneseqr.emb1.NA1993.DAT:
/SIDS2/gcgdata/geneseqr.emb1.NA1995.DAT:
/SIDS2/gcgdata/geneseqr.emb1.NA1995.DAT:
/SIDS2/gcgdata/geneseqr.emb1.NA1995.DAT:
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SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS2/gcgdata/geneseg/genesegn-embl/NA1983.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA1984.DAT:*/SIDS2/gcgdata/geneseg/genesegn-embl/NA1985.DAT:*
                                                                                            8, 2003, 00:43:28 ; Search time 131.941 Seconds
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:
                                                                                                                                                                                                                                                                         4370478
            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                         hits satisfying chosen parameters:
                                                                                                                                                                                                                                              2185239 seqs; 1125999159 residues
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                                                                  nucleic search, using sw model
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ABV23433
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AAZ28810
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Gapop 10.0 , Gapext 1.0
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Maximum Match 1008
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Sequences AA228811-228827 represent probes for detecting the rat membrane metalloprotease designated neprilysine II (NEPII) gene (AA228810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic- hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence represents the gene for the rat membrane metalloprotease
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              P II, involved in proteolysis of
used to screen for inhibitors;
e.g. cardiovascular disease
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Pred. No. 0.29;
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              New membrane metalloprotease NEP II, neuronal and hormonal peptides, used potentially useful for treating e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 12-16; 29pp; French.
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                   Claim 3; Page 23;
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                                                                                                                                                                                                                                                                            disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD) (e.g. female sexual arousal ar
disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine disorders.
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                                                                                                                                                                                                                                                      Gaps
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MED; female sexual dysfunction; FSD; female sexual arousal disorder;
FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted endopeptidase; SEP; endocrine; vasotropic; analgesic;
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                                                                                                                                          Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;
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/note- "Encodes catalytic domain"
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                                                                                                                                                                                                DB 20;
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Pred. No. 0.55;
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                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                        1760 CCCGAAGTTTCTTGAGGCTCC 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1664..2286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6; 167pp; English.
                                                                                                                                                                                                                                                                                                         1 CCCGAAGTTTCTTGAGGCTCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walsh RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВЪ.
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                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD28130 standard; DNA; 2286
                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUL-2001; 2001WO-IB01263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-2000; 2000GB-0017387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stacey P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-155042/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200206492-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harrow ID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD28130;
                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
AAD28130/c
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Length 2925;

DB 21;

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Query Match
Best Local S
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                                                                                                                                       KESULT 5
ABV23433
                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metallopeptidase-like enzyme, designated NL-1. The specification also describes NL-2 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimeric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "neutral endopeptidase metallopeptidase-like enzyme NL-1"
                                                                                                                                                                                                                                                                                                                                                                NEP-like enzyme; protein production; protein secretion; neurological disease; Alzheimer's disease; pain; psychiatric disorder; fertility; bone disease; abnormal phosphate metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. Nu enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to boses, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide
                                                                              Gaps .
                                                                                                                                                                                                                                                                                                                  CDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
                                                                                                                                                                                                                                                                                                                                               endopeptidase metallopeptidase-like enzyme;
                                                                            ;
0
                                          Score 19.4; DB 24; Length 2286; Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present sequence encodes a murine neutral endopeptidase
                                                                            1; Indels
                Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;
                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
332..2629
                                                                                                                          1622 CCCGAAGCTTCTTGAGGCTCC 1602
                                                                                                           1 CCCGAAGTTTCTTGAGGCTCC 21
                                                                                                                                                                                                     AAA63763/c
ID AAA63763 standard; cDNA; 2925 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    processing by the NL-3 enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desgroseillers L, Boileau G;
                                            ch 92.4%;
1 Similarity 95.2%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-FEB-2000; 2000WO-CA00147.
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                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYMO-) UNIV MONTREAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-549148/50.
                                                                                                                                                                                                                                                                                                                                                 Neprilysin; neutral
                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAB08130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200047750-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-1999;
                                                                                                                                                                                                                                                                                   04-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-2000
                                                                                                                                                                                                                                                      AAA63763;
                                                                                                                                                                                                                                                                                                                                                                                                                               Wus sp
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
                                                                                                                                                                                         RESULT 4
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selecting a composition for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assessing the prostate cell carcinogenic potential of a compound, determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.8; DB 23;
Pred. No. 23;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prostate expression marker cDNA 23424
                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
92.4%; Score 19.4; 95.2%; Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 4269; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan JE;
                                                                                                                                 1958 CCCGAAGCTTCTTGAGGCTCC 1938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGAAGTTTCTTGAGGCTCC 21
                                                                                                 21
                                                                                                                                                                                                                                                                                  ABV23433 standard; cDNA; 1746 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmacogenomic marker; gene; ss.
                                                                                                    1 CCCGAAGTTTCTTGAGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.8%;
Llarity 90.5%;
Conservative (
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2000US-207454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-2000; 2000US-211314P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endege WO,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 19; Conserv
                       1 Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L7-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                    ABV23433;
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anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoprosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple solerosis; Alzheimer's disease; neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; scerebrovasospasm;

Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;

Nucleotide sequence of a human metalloprotease enzyme IGS5.

23-JUL-2001 (first entry)

AAF89737

subarachnoid hemorrhage; cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea, inflammation; chemotherapy induced injury; tumour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia; Huntington's disease;

de la Tourette's syndrome; ss

Homo sapiens.

/product= "metalloprotease enzyme IGS5"

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1..2076 /*tag=

Location/Qualifiers

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Weske

Deleersnijder W. Wiegers R,

WPI; 2001-343815/36. P-PSDB; AAB83840.

(SOLV) SOLVAY PHARM BV.

99EP-0203862.

2000EP-0201937 2000NL-1015356

31-MAY-2000; 31-MAY-2000; 19-NOV-1999; 9-NOV-1999;

17-NOV-2000; 2000WO-EP11532

WO200136610-A1

25-MAY-2001.

9 09:32:27 2003

Wed Jul

1525 CCCGAAGCTTCCTGAGGCTCC 1545

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                      Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1746 BP; 299 A; 531 C; 580 G; 336 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.8%; Score 17.8; DB 23; 90.5%; Pred. No. 23; ive 0; Mismatches 2;
                                                                                                                                    Human prostate expression marker cDNA 29281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 6257; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monahan JE;
                                                                                                                                                                                        pharmacogenomic marker; gene; ss.
                               ABV29290 standard; cDNA; 1746 BP.
                                                                                                                                                                                                                                                                                                                                                                                           2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                             2000US-183319P
                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2000; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                           20-FEB-2001; 2001WO-US05171
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 84.8 Best Local Similarity 90.5 Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer in a patient;
                                                                                                                                                                                                                                                        WO200160860-A2
                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                              6-MAR-2000;
5-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000;
                                                                                                   .6-SEP-2002
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                                                                                                                                                                                                                                                                                         23-AUG-2001
                                                                   ABV29290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patient;
RESULT 6
                 ABV29290
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The present sequence encodes a human metalloprotease enzyme designated 1GSS polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, ParkInson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, behign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infarction, peripheral vascular disease, Raynaud's disease, kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis, cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New IGS5 polypeptides useful for treating infections, pain, cdiabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2076 BP; 493 A; 578 C; 636 G; 369 T; 0 other
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Gaps

. 6

Indels

ò g AAF89737/c ID AAF89737 standard; DNA; 2076 BP

RESULT 7

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                           Gaps
                           ö
       Length 2076;
                           Indels
        DB 22;
                           0; Mismatches
        Score 17.8;
                  Pred. No.
                                                         1405 CCCGAAGCTTCCTGAGGCTCC 1385
                                              1 CCCGAAGTTTCTTGAGGCTCC 21
        84.8%;
Query Match
Best Local Similarity 90.5%
19; Conservative
                                              δ
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AAS97186 standard; cDNA; 2232 BP RESULT 8
AAS97186/C
ID AAS9718

AAS97186;

26-FEB-2002 (first entry)

protease; PCR primer; cytostatic; immunomodulator; cardiant; Human metalloprotease partial DNA sequence #15

vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic; anorectic; antiinflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoietic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; psychotic disorder cognition disorder; hypotension; hypertension; psychotic d dyskinesia; metabolic disorder; inflammatory disorder; ss.

WO200183782-A2

08-NOV-2001

04-MAY-2000; 2000US-201879P.

SUGE-) SUGEN INC.

Caenepeel S; Sudarsanam S, Manning G, Plowman GD, Whyte D, Payne V;

WPI; 2002-041502/05. P-PSDB; AAU72903 Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, cardiovascular disease, migraine, pain, psychotic and inflammatory

Claim 30; Figure 1R-S; 232pp; English.

The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering S (which modulates protease activity in vitro) may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood brain, ovarian, bladder or kidney), immune related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAS97159-AAS97195 represent human protease coding sequences and primers of the invention.

Sequence 2232 BP; 512 A; 620 C; 705 G; 395 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple sclerosis; Alzhelmer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peripheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human metalloprotease enzyme designated
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm;
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Score 17.8; DB 24; Length 2232;
Pred. No. 24;
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diabetes, obesity, anorexia, bulimia, asthma, schizophrenia,
hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of a human metalloprotease enzyme IGS5
                                                                                        Indels
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                                                  Pred. No. 24;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de la Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 8-9; 115pp; English.
                                                                                                                                                                                                                          1561 CCCGAAGCTTCCTGAGGCTCC 1541
                                                                                                                                                                                1 CCCGAAGTTTCTTGAGGCTCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF89739 standard; DNA; 2262 BP.
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            84.8%;
90.5%;
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2000EP-0201937.
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            Ouery Match 84.8
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SOLV ) SOLVAY PHARM BV
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P-PSDB; AAB83842.
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Todd

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Human; protease; PRTS-13; enzyme; gastritis; cirrhosis; Crohn's disease; gastrointestinal disorder; autoimmune; inflammatory; cell proliferative; cardiovascular; developmental; epithelial; neurological; reproductive; AIDS; Acquired Immune Deficiency Syndrome; allergy; rheumatoid arthritis; anaemia; asthma; atherosclerosis; hypertension; myocardial infarction; hepatitis; cancer; psoriaais; Oushing's syndrome, hypothyroidism; eczema; epilepsy; Alzheimer's disease; Huntington's disease; Parkinson's disease; pick's disease; infertility; vitiligo; drug screening; gene therapy; ss.
psychotic and neurological disorders, autism, multiple sclerosis, Alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis. scenbral infarction, peripheral vascular disease, Raynaud's disease, kidney diseases, gastroinfestinal disorders, mortlity disorders and conditions of delayed gastric emptying, post-operative or disbectic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, inmune disorders, arthritis, endotoxin shock, sepsis, compilications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                    Gaps
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Kallick DA, Nguyen DB, Lee EA, Khan FA;
tiffin JA, Policky JL, Ramkumar J, Yang J
Kearney L, Baughn MR, Borowsky ML;
                                                                                                                                                                                                                                             Score 17.8; DB 22; Length 2262;
Pred. No. 24;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                              Sequence 2262 BP; 520 A; 628 C; 716 G; 398 T; 0 other;
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Tribouley CM, Das D, Kallick DA, Nguye
Yue H, Au-Young J, Griffin JA, Policky,
Thangavelu K, Ding L, Kearney L, Baugh
                                                                                                                                                                                                                                                                                                                                        1591 CCCGAAGCTTCCTGAGGCTCC 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                84.8%;
90.5%;
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2000US-223544P.
2000US-224717P.
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428..1648
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Matches 19; Conservative
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04-AUG-2000;
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16-AUG-2000;
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The invention relates to an isolated human protease polypeptide (PRTS).

PRTS protein and DNA are useful for diagnosing, treating and preventing gastrointestinal disorders (gastriits, cirrhosis, crohn's disease), cardious and disorders (ALDS, allergy, rheumatch arthritis, anaemia, asthma), cardiovascular disorder (atherosclerosis, hypertension, myocardial infarction), call proliferative disorders (heptitis, cancer, psoriasis), developmental disorders (Carative disorders (Peptitis, cancer, psoriasis), developmental disorders (Carative disorders), neurological disorders (epithelial disorder (vitiligo, keloid, eczema), neurological disorders (Parkinson's disease, pick's disease, Huntington's disease, protein is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PRTS DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy and in microarrays cutilising fluids or tissues from patients to detect altered PKIN
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                                                                                                                       New human protease polypeptide, useful in diagnosis, prevention and treatment of gastrointestinal, cardiovascular, autoimmune/inflammatory, call proliferative, developmental, epithelial and neurological disorders
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inflammation; chemotherapy induced injury; tumour invasion;
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subarachnoid hemorrhage; cerebral ischemia; cerebral infarction;
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  ree S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression. The present sequence is human PRTS-13 cDNA.
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  Lal
Sanjanwala MS, 'Yao MG, Burford N, Walia NK, I
Lo TP, Tang YT, Elliott VS, Azimzai Y, Lu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.8; DF
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                                                                                                                                                                                                                                Claim 5; Page 174-175; 182pp; English.
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90.5%;
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mes 19; Conservative
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                                                               WPI; 2002-206082/26.
                                                                                  P-PSDB; AAE19176
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Matches
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Use of an inhibitor of neuropeptide Y in the preparation of medicament for the treatment or prevention of male erectile dysfunction
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                                                                                                                     /partial .
/note= "the CDS does not include a stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             such as obesity, bulimia, anorexia and metabolic disorders
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/note* "the 3' end of the sequence is miss
from Figure 8 of the specification'
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                       partial vector sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wayman CP;
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AAF59660/c
ID AAF59660 standard; cDNA; 2636 BP
                                                                                           /product= "SEP'
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2001GB-0009910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PFIZ ) PFIZER LTD. (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 19; Conserv
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                                                                                                                                                                                                                                                                                                 WO200247670-A1
                                                                                                                                                                         misc_feature
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23-APR-2001;
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                    EXEXEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            urinary retention, osteoporosis, angina perforis, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, alzhelmer's disease, and other neurodegenerative diseases, sleep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, Kidney diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastropareals, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence encodes a human metalloprotease enzyme designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulinia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        male sexual dysfunction; male erectile dysfunction; obesity;
anorexia; bulimia; vasotropic; anorectic; therapy; inhibitor; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isorder, epilepsy, cardiovascular diseases, arteriosclerosis, erebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.8%; Score 17.8; DB 22; Length 2340;
llarity 90.5%; Pred. No. 24;
Conservative 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                      9-NOV-1999; 99NL-1013616.
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                                                                                                             17-NOV-2000; 2000WO-EP11532
                                                                                                                                                                                                                                       31-MAY-2000; 2000NL-1015356
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             WO200136610-A1
                                                              25-MAY-2001.
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misc_feature
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Gaps

ABN84280;

ABN84280/c

Query Match

Best Loc Matches

δ g

respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic; cerebroprotective; hypotensive; cytostatic; antiinflammatory; Human; SNEPb; neprilysin-like membrane metallopeptidase; splice variant; alternative splicing; zinc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain; hypertension; cancer; inflammation; cardiovascular disease; neuronal disease; pancreatic disease; cardiovascular; hepatotropic; ss. Homo sapiens.

EP1069188-A1

17-JAN-2001.

99EP-0401767. 15-JUL-1999;

99EP-0401767. 15-JUL-1999;

(SNFI) SANOFI-SYNTHELABO

Jagerschmidt A, Agnel M, Culouscou J;

WPI; 2001-212582/22. P:PSDB; AAB60562.

New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal and hepatic ischemia

Claim 5; Page 30-33; 72pp; English.

as research reagents and material for the discovery of treatments and diagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPa, SNEPD or SNEPc. Such antibodies are used to isolate or identify clones expressing the protein, or to purify the proteins by affinity chromatography. SNEP proteins may also be used in screening for compounds which modulate. SNEP endopeptidase activity, and to assess enzymatic cleavage of small molecule substrates in cells, cell-free preparations, chemical libraries The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP nucleotides may be used as hybridisation probes for cDNA and genomic DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa, SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues; and product mixtures. The SNEP proteins (as vaccine compositions), SNEP nucleotides, and SNEP activators or inhibitors may used to treat acute and chronic renal insufficiency, renal and hepatic

Sequence 2636 BP; 601 A; 759 C; 813 G; 462 T; 1 other;

DB 22; Length 2636; Indels .; 7 Pred. No. 25, 0; Mismatches Score 17.8; 84.8%; illarity 90.5%; Conservative Ouery Match Best Local Similarity Matches 19; Conserv

Gaps

AAF59661 standard; cDNA; 2663 BP RESULT 14 AAF59661

AAF59661;

27-APR-2001 (first entry)

Human neprilysin-like membrane metallopeptidase SNEPc cDNA.

neuronal disease; pancreatic disease; prostatic disease; respiratory disease; gene therapy; nephrotropic; vasotropic; analgesic; cerebroprotective; hypotensive; cytostatic; antiinflammatory; splice variant; alternative splicing; zinc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia; pain; hypertension; cancer; inflammation; cardiovascular disease; neprilysin-like membrane metallopeptidase; cardiovascular; hepatotropic; ss. SNEPC;

333

Homo sapiens.

EP1069188-A1.

17-JAN-2001.

99EP-0401767. 15-JUL-1999;

P.F.

(SNFI) SANOFI-SYNTHELABO.

15-JUL-1999; 99EP-0401767

Culouscou J; Agnel M, Jagerschmidt A,

WPI; 2001-212582/22. P-PSDB; AAB60563. New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal and hepatic ischemia

Claim 5; Page 35-38; 72pp; English.

8 % 5 5 5

The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the cDNAs encoding them. SNEPa and SNEPc are neprilyshin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP nucleotides may be used as hybridisation probes for cDNA and genomic DNA; to isolate full-length cDNAs and genomic clones encoding SNEPa, diagnostics for animal and human diseases; and for chromosome identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPs, SNEPb or SNEPc. Such antibodies are used insolate or identify clones expressing the protein, or to purify the proteins by affinity chromatography.

SNEP proteins may also be used in screening for compounds which modulate cell-free preparations, chemical libraries. ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, as well as cardiovascular, neuronal, pancreatic, prostatic, renal, peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnormal expression of SNEPa, SNEPb or SNEPc. The present sequence represents SNEPD or SNEPc; to isolate CDNA and genomic clones of SNEP homologues; as research reagents and material for the discovery of treatments and SNEP endopeptidase activity, and to assess enzymatic cleavage of smal respiratory or hepatic diseases. they may also be used in modulating and product mixtures. The SNEP proteins (as vaccine compositions), SNEP nucleotides, and SNEP activators or inhibitors may used to treat acute and chronic renal insufficiency, renal and hepatic molecule substrates in cells,

radation in the brain or kidney or in or treat any disorder related to abnormal

peptide activation and/or degradation in

organ, or to diagnose

CDNA encoding SNEPb

expression

of SNEPa, SNEPb or SNEPc. The present sequence represents

ischaemia, pain, stroke, hypertensive disease, cancer, inflammation, well as cardiovascular, neuronal, pancreatic, prostatic, renal, well as cardiovascular, neuronal, pancreatic, prostatic, renal, respiratory or hepatic diseases they may also be used in modulating

1598 CCCGAAGCTTCCTGAGGCTCC, 1578 CCCGAAGTTTCTTGAGGCTCC 21

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cDNA encoding SNEPc.
SXS
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Sequence 2663 BP; 609 A; 769 C; 816 G; 468 T; 1 other;

Gaps ö Length 2663; Indels Score 17.8; DB 22; Pred. No. 25; 0; Mismatches 84.8%; 90.5%; Query Match
Best Local Similarity 90.5%,
...hes 19; Conservative

1 CCCGAAGTTTCTTGAGGCTCC 21

δ q

1625 CCCGAAGCTTCCTGAGGCTCC 1605

RESULT 15

AAA63764/C ID AAA63764 standard; cDNA; 2676 BP.

AAA63764;

(first entry)

04-DEC-2000

cDNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-2.

NEP-like enzyme; protein production; protein secretion; neurological disease; Alzheimer's disease; pain; psychiatric disorder; fertility; bone disease; abnormal phosphate metabolism; ss. Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;

Homo sapiens

Location/Qualifiers Key

/*tag= a /product= "neutral endopeptidase metallopeptidase-like enzyme NL-2" ..2319

WO200047750-A2.

17-AUG-2000.

11-FEB-2000; 2000WO-CA00147.

99CA-2260376 11-FEB-1999;

UYMO-) UNIV MONTREAL

Boileau G; Desgroseillers L,

WPI; 2000-549148/50.

P-PSDB; AAB08131

Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders

Disclosure; Fig 4; 59pp; English

The present sequence encodes a human neutral endopeptidase metallopeptidase-like enzyme, designated NL-2. The specification also describes NL-1 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimeric constructs containing the foreign protein are have been localised to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide the NL-3 enzyme.

Sequence 2676 BP; 608 A; 771 C; 823 G; 474 T; 0 other;

Gaps ô Length 2676; Indels DB 21; ; 7 Score 17.8; DB Pred. No. 25; 0; Mismatches 84.8%; ilarity 90.5%; Conservative Query Match Best Local Similarity Matches 19; Conserv

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4: /cgn2_6/ptodata/1/ina/FB_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		US-08-961	-09-522-217-55	-08-790-912	-08-961-527	US-08-961	US-08-832-883	08-832	09-134	-08-117	US-08-015-973-	US-08-448-164	US-09-816-703A	US-09-103-840A	US-09-103-840A	US-09-118-442-2	US-09-677-064	-949-861-676-	227	09-597	324	18 - 384	08-904	19-315	31	-08-727	38-727	-08-324
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7863 7863 7863 7917 7917 7917 7917 7917 9030 9030 9416 9416 9416 9595 825		ub
		c ac dc near ity serv
	LOLOLD ROLLE B GROSEZ OHZ W DHYOSO .	S: S: on
	T 1 -961-083-91/c enence 91, Applicat. enence 91, Applicat. enence 91, Applicat. APPLICANT Chol e' REAL INFORMATION: APPLICANT Chol e' CORRESPONDENCE ADD STREET: 9410 Ke COUNTRY: ROCKVILLE STREET: 9410 Ke COUNTRY: BADD CONPUTER READABLE MEDIUM TYPE: DI CORPUTER: HP VE OPERATING SYSTEM SOFTWARE: APPLICATION REPERENCE/ACENT INF REFERENCE/ACENT INF REFERENCE/ACENT TELEPHONE: (301)	BE I
$ \infty \infty$	Handler Branch B	- DOE 4
	1 10061-083-91/ 1006	TYPE: n STRANDED TOPOLOGY 161-083-9 ' Match Local S1
		TY ST 100 100 100 100 100 100 100 100 100 10
2002 2002 2003 2003 2003 2003 2003 2003	RESULT 1 US-08-961-0 Sequence Patent NG GENERAL APPLIC TITLE COMPUT COMP	S S S S S S S S S S S S S S S S S S S
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Sequence 26, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INFORMINS: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(1..30, 34..39, 46..51, 55..99, 103..135, 139
.153, 157..165, 169..186, 190..210, 217..225,
229..234, 238..6150, 6154..6177, 6181..6201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 77.1%; Score 16.2; DB 2; Length 6201; Best Local Similarity 85.7%; Pred. No. 22; Matches 18; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3:50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
APPLICATION NUMBER: US 60/026,939
FILING DATE: 23.5EP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Leary, Kathryn
REGISTRATION NUMBER: 36,317
REPERNEK/POCKET NUMBER: 7600-401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                               TELEX: 831-494
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEPHONE: (301) 309-8512
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
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LOCATION:
US-08-790-912-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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Patent No. 5976542
GENERAL INFORMATION:
APPLICANT: Welser, Jeffrey N.
APPLICANT: Plaut, Andrew G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT
TITLE OF INVENTION: OF STREPTOCOCCUS PNEUMONIAE INFECTION
NUMBER OF SEQUENCES: 10.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-01
SARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTERQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 Market Street, 36th Floor CITY: Philadelphia STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 16.2; DE; DE; Pred. No. 20; 0; Mismatches
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FILING DATE: 29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506 CCCGAAGATTCCTGAGGATCC 526
                                                                            Sequence 55, Application US/09522217 Patent No. 6307024
                                                                                                                                                   APPLICANT: No. 6307024ak, Julia E. APPLICANT: Presnell, Scott R. APPLICANT: Sprecher, Cindy A. APPLICANT: Foster, Donald C. APPLICANT: Holly, Richard D. APPLICANT: Gross, Jane A. APPLICANT: Johnston, Janet V. APPLICANT: Nelson, Andrew J. APPLICANT: Dillon, Stacey R. APPLICANT: Dillon, Stacey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 77.1%;
Best Local Similarity 85.7%;
Matches 18; Conservative
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PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (54)...(491)
US-09-522-217-55
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RESULT 3

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Baldi, Alphonso
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                                                                                  ADDRESSEE:
STREET: S
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APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                   Length 15213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 30;
                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.50 inch, 1.4Mb storage
                                                                                                                   DB 4;
                                                                                                               Score 16.2; DB
Pred. No. 25;
0; Mismatches
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Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                  E: Human Genome Sciences, Inc. 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                     5337 CCCGCAGTTTCTTGAGCATCC 5357
                                                                                                                                                                                                                                                                                      Sequence 317, Application US/08961083
Patent No. 6159469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52, Application US/08832883 Patent No. 5807681
                                                                                                                                                                                   1 CCCGAAGTTTCTTGAGGCTCC 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE, DOOKET NUMBER: PB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Giordano, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.4%;
                                                                                                                   77.18;
85:78;
                 : 15213 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                                                  18; Conservative
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                   RESULT 5
US-08-961-083-317/c
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                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                 ; TOPOLOGY:
US-08-961-527-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-961-083-317
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Gaps
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Patent No. 5840506
GENERAL INFORMATION:
APPLICANT: Giordano, Antonio
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF TITLE OF INVENTION: CANCER
METHODS FOR THE DIAGNOSIS AND PROGNOSIS OF CANCER: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 889;
                                                                                                                     E: SEIDEL, GONDA, LAVORGNA & MONACO, P.C. Suite 1800 Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S: SEIDEL, GONDA, LAVORGNA & MONACO, P.C. Suite 1800 Two Penn Center Plaza
                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.30
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Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/832,883
                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 CCGAAGTTTCTTTAAGCTTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MORACO. Daniel A
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 831
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Monaco, Daniel A
REGISTRATION NUMBER: 30,480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: DNA (genomic) US-08-832-883-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
72.4%;
Best Local Similarity 85.0%;
Matches 17; Conservative Cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 52
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 889 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                        TITLE OF INVENTION: ME
TITLE OF INVENTION: OF
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Sulle
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                                                                                                                                                                      Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
NUMBER OF SEQUENCES: 9
      OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 PURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.2;
Pred. No. 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1155 Avenue of the Americas
                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: CORSTANDE, BRAHM J.
REGISTRATION NUMBER: 34,804
REFERENCE/DOCKET NUMBER: 4518R26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (513) 627-0269
                                                                       APPLICATION NUMBER: US/08/117,373
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,973
ELING DATE: 10-FEB-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        · 915 CAGAGGTTTCTGGAGGCTCC 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PENNIE & EDMONDS
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212)869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.4%;
                                                                                                                                                                                                                                     TELEPHONE: (513) 627-2858
TELEFAX: (513) 627-0260
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                            LENGTH: .3914 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6924 base pairs
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Best Local Similarity 85.0°
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                         linear
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10036-2711
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APPLICANT: WAMRZYNIAK, CYNTHIA J
TITLE OF INVENTION: ISOLATED HAIR KERATIN GENES AND THEIR
TITLE OF SEQUENCIAL USE IN HAIR GROWTH ACTIVE IDENTIFICATION ASSAYS
WUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATIN
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILLING DATE: 1998-08-13
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                                                                                                                                                                                                                                                               Score 15.2; DE
Pred. No. 54;
0; Mismatches
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  REFERENCE/DOCKET NUMBER: 8321-13 US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1055, Application US/09134001C
Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Staphylococcus epidermidis US-09-134-001C-1055
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                                                                                                                                                                                                                                                                                                                                               2 CCGAAGTTTCTTGAGGCTCC 21
                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-832-877-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.4%;
85.0%;
                         (215) 568-8383
(215) 568-5410
                                                  TELEFAX: (215) 568-5549
INFORMATION FOR SEQ ID NO: 52
SEQUENCE CHARACTERISTICS:
LENGTH: 889 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                               Query Match 72.4%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 85.0%
Matches 17; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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) OTHER INFORMATION: "n" bases at various positions throughout the sequence

) OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2
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APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SECUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4403765;
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0
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    APPLICANT: Melcher, Thorsten
APPLICANT: Mueller, Sabine
APPLICANT: Mueller, Sabine
APPLICANT: Chin, Daniel
TITLE OF INVENTION: Use of Protein Tyrosine Phosphatase Zeta as
TITLE OF INVENTION: Treatment and Visualization of Brain Tumors
FILE REFERENCE: 262/235 AGY
CURRENT APPLICATION NUMBER: US/09/816,703A
CURRENT FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                              Length 7941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 76;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4203085 CCGAGGTTTCTCGATGCTCC 4203066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1895 CTGAAGATTCTTCAGGCTCC 1914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.4%;
Best Local Similarity 85.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (148)..(7092)
US-09-816-703A-1
                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FLEISCHMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 17; Conserv
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LENGTH: 4403765
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US-09-103-840A-1/c
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                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 7941
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                                                                                                     Gaps
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                                                            Length 6924;
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASE-BETA
                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                     0; Mismatches
                                                          Query Match 72.4%; Score 15.2; Best Local Similarity 85.0%; Pred. No. 74 Matches 17; Conservative 0; Mismatche
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/448,164
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: US 08/015,973
FILING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                     Sequence 1, Application US/09816703A Patent No. 6455026
                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08448164
Patent No. 5925536
GENERAL INFORMATION:
                                                                                                                                              2 CCGAAGTITCITGAGGCICC 21
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212)869-8864/9741
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Best Local Similarity 85.0%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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1..6924
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JS-08-448-164-2
; LOCATION:
US-08-015-973-2
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Gaps

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Gaps
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: 05/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                      Query Match 72.4%; Score 15.2; DB 4; Length 4411529; Best Local Similarity 85.0%; Pred. No. 64; Matches 17; Conservative 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.5%; Score 14.8; D
Best Local Similarity 88.9%; Pred: No. 84;
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/055,446
EARLIER FILING DATE: 1997-08-11
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-07-28
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/118,442B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4210838 CCGAGGTTTCTCGATGCTCC 4210819
                                                                                                                                                                                                             TYPE: DNA ORGANISM: MYCODACTETIUM tuberculosis OFGANISM: MYCODACTETIUM tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/09118442B Patent No. 6197561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(685)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Martino-Catt, Susan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 · 3 CGAAGTTTCTTGAGGCTC 20
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Wang, Xun
                                                                                                                                                                                              LENGTH: 4411529
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                                                                                                                                                                                                                                                                                         US-09-103-840A-1
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LENGTH: 685
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Search completed: July 8, 2003, 09:32:29 Job time: 41.0402 secs

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July 8, 2003, 19:09:54; Search time 121.288
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                  1105431 seqs, 789497651 residues
                                                                            OM nucleic - nucleic search, using sw model
                                                                                                                                                                                           US-09-647-780A-18
21
1 cccgaagtttcttgaggctcc 21
                                                                                                                                                                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                               Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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		Sequence 4, Appli	1, App]	5, App	5, Ap	91, A	24415,	55, Ap	55, A	46, A	3, Ap	344,	4, Appl.	48, AF	175,	359,	317,	788, 1	29893,	13668	
	Description	ence (Sequence	Sequence 5,	Sequence	Sequence 91,	Sequence 24415	Seguence 55	Sequence	Sequence	Sequence	Sequence 344,	Sequence 4	Sequence 48,	Seguence	Sequence	Sequence	Sequence 788,	Sequence 29893	Sequence	
	Descr	Sedu	Sed	Sedu	Sed	Sed	Sedn	Sedn	Sed	Sed	Sec	Sec	Sedu	Sedi	Sec	Sec	Sec	Sedr	Sedı	Sec	
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		-017-2	US-09-905-846-1	JS-10-017-273A-	US-09-905-846-	US-09-765-272-9	15-09-918-995-2441	JS-10-295-723-55	US-09-923-246-55	US-09-825-561A-46	JS-09-949-654-3	US-09-770-696-34	18-10-051-307-4	JS-09-938-842A-48	US-09-960-253-175	JS-10-044-090-359	JS-09-765-272-31	IS-09-933-797-788	15-09-918-995-29893	US-09-878-574-13668	
	A	US-10-017-273A-4	0S-0	JS-10-	us-0	ns-0	.60-SD	US-10.	ns-0	ns-0	ns-0	ns-0	US-10	60-SD	ns-0	us-1(ns-0	60-Sn	60-Sn	ns-0	
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	Length DB	2893	2893	2975	2975	199	508	3072	3072	3072	368004	171	1175	2979	7497	7792	30	213	258	301	
æ	Query Match	84.8	84.8	84.8	84.8	77.1	77.1	77.1	77.1	77.1	75.2	73.3	73.3	73.3	73.3	73.3	72.4	72.4	72.4	72.4	
	Score	17.8	17.8	17.8	17.8	16.2	16.2	16.2	16.2	16.2	15.8	15.4	15.4	15.4	15.4	15.4	15.2	15.2	15.2	15.2	
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Sequence 33959, A	Sequence 358, App	Sequence 378, App	Sequence 19894, A	Sequence 1904, Ap	Sequence 1905, Ap	Sequence 20, Appl		Sequence 1901, Ap	Sequence 1903, Ap		Sequence 8518, Ap	Seguence 5, Appli	Sequence 1812, Ap	Sequence 3, Appli	Sequence 1673, Ap	Sequence 10, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 17459, A	Sequence 671, App	Sequence 1710, Ap	Sequence 168, App	Sequence 155, App	Sequence 5392, Ap	Sequence 3535, Ap	
Sed	Sedr	Sedi	Sedı	Sedi	Sedi	. Sed	Se	Sedi	Seg	Sed	Sed	Sed	Se	Sed	Se	Sed	Sed	Sed	Šē	Se	Se	Sed	Se	. Se	Se	
US-09-918-995-33959	US-09-991-936-358	US-09-991-936-378	US-09-918-995-19894	US-09-991-936-1904	US-09-991-936-1905	US-09-746-783-20	. US-09-764-864-108	US-09-991-936-1901	US-09-991-936-1903	US-09-822-846-209	US-09-764-891-8518	US-09-983-000A-5	US-09-954-456-1812	US-09-983-000A-3	US-09-764-864-1673	US-09-953-611-10	US-09-901-152-3	US-09-939-964-1	US-09-864-761-17459	US-09-864-761-671	US-09-974-300-1710	US-09-822-846-168	US-09-729-674-155	US-09-923-876-5392	US-09-880-107-3535	
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72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	72.4	71.4	71.4	71.4	71.4	71.4	70.5	70.5	
15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	15.2	. 15.2	15.2	15.2	15.2	15.2	15	10	15	15	15	14.8	14.8	
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ALIGNMENTS

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :

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                                                                                                                 Treatment of Male Sexual Dysfunction
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                                                                                                                                                RRENT APPLICATION NUMBER: US/10/017,273A
                                                                                                                                                                                                                                                                                                    G DATE: 2001-08-24
CATION NUMBER: US 09/905,846
                                                                                                                                                                                                                                                                                                                                                     CATION NUMBER: US 60/291,722
                                                                                                                                                                                 NUMBER: US 60/265,358
                                                                                                                                                                                                             ION NUMBER: GB 0030647.2
                                                                                                                                                                                                                                                                                   CATION NUMBER: GB 0120679.6
                                                                                                                                                                                                                                       S DATE: 2000-12-15
SATION NUMBER: GB 0108730.3
Application US/10017273A
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Best Local Similarity 90.5%;
Matches 19; Conservative
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                                                                                                                                                                                                     001-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
US-10-017-273A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 2893
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE
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APPLICANT: Choi et. al.
IIILE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                         APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
APPLICANT: Roderick Thomas Walsh
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE: REFERENCE: PCS10926APM
CURRENT APPLICATION NUMBER: US/09/905,846
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/220,908
PRIOR APPLICATION NUMBER: 60/220,908
PRIOR APPLICATION NUMBER: 60/220,908
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEO ID NOS: 8
SOFTWARE: FastSEO for Windows Version 4.0
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ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
SOFTWARE: ASCII Text
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.8; DE
Pred. No. 12;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
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                        1918 CCCGAAGCTTCCTGAGGCTCC 1898
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Patent No. US20020061545A1
GENERAL INFORMATION:
1 CCCGAAGTTTCTTGAGGCTCC 21
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                                                                                                                                                               Sequence 5, Application US/09905846 Patent No. US20020102707A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION
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Best Local Similarity 90.5%;
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                       APPLICANT: Ian Dennis Harrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-765-272-91/c
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LENGTH: 2975
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US-09-905-846-5
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                                                                                                                                                          APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
TITLE REFERENCE: PCS10926APME
CURRENT APPLICATION NUMBER: 0S/09/905,846
CURRENT FILING DATE: 2001-07-13
PRIOR PELING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-26
PRIOR FILING DATE: 2000-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 2893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLICANT: Naylor, Alasdair M.
PLICANT: Van Der Graaf, Plecer H
LLCANT: Wan Der Graaf, Plecer H
LLCANT: Wayman, Christopher P.
LE OF INVENTION: Treatment of Male Sexual Dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches.
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICATION NUMBER: US 09/905,846
FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR APPLICATION NUMBER: US 60/291,722 OR FILING DATE: 2001-05-17 OR APPLICATION NUMBER: US 09/895,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IOR APPLICATION NUMBER: US 60/265,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-31
PAPLICATION NUMBER: GB 0030647.2
FILING DATE: 2000-12-15
APPLICATION NUMBER: GB 0108730.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-04-06
APPLICATION NUMBER: GB 0120679.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCCGAAGITICITGAGGCICC 21
                                                                Sequence 1, Application US/09905846 Patent No. US20020102707A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.8%;
90.5%;
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-06-29
                                                                                                                GENERAL INFORMATION:
APPLICANT: Ian Dennis Harrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 90.5
Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
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FNGTH: 2893
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CURRENT APPLICATION NUMBER: US/09/923,246
CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
PRIOR FILING DATE: BARLIER FILING DATE: 2000-03-09
PRIOR PAPPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
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DATE: 1999-03-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hammond, Angela K. FILLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                           DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                         Score 16.2; E
Pred. No. 82;
0; Mismatches
                                                PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US. 60/142, 013
PRIOR FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 55
LENGTH: 3072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 CCCGAAGATTCCTGAGGATCC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09923246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: EARLIER FILING PRIOR APPLICATION NUMBER: EARLIER
                                                                                                                                                                                                                                                                                                                                                           77.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnston, Janet V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nelson, Andrew J
Dillon, Stacey R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (54)...(491)
US-09-923-246-55
                                                                                                                                                                                                                                                                                            ; LOCATION: (54)...(491)
US-10-295-723-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
US-09-825-561A-46
                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                                            Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
                                                                                                                                                                                            DB 10;
                                                                                                                                                                                         Score 16.2; DE
Pred. No. 67;
Wismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16.2; DI
Pred. No. 72;
0; Mismatches
                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 91: US-09-765-272-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24415
LENGTH: 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: No. US20030125524Alak, Julia E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24415, Application US/09918995
Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CCCGAAGTTTCTTGAGGCTCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 CCAGAGGTTTCTTGAGTCTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55, Application US/10295723
Publication No. US20030125524A1
                                                                                                                                                                                                                                                                                 1 CCCGAAGTTTCTTGAGGCTCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(508)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                        21 CCCGCAGTTTCTTGAGCATCC 1
                                           LENGTH: 199 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
INFORMATION FOR SEQ ID NO: 91: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnston, Janet V.
Nelson, Andrew J.
Dillon, Stacey R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Presnell, Scott R.
Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
                                                                                                                                                                            Query Match
Best Local Similarity 85./*
"hea 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-918-995-24415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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g δλ

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APPLICANT: SHI, LIFANG
APPLICANT: HOOKER, BRIAN S.
TITLE OF INVENTION: GENE PROMOTERS ISOLATED FROM POTATO AND USE THEREOF
FILE REFERENCE: 05944405411
CURRENT APPLICATION NUMBER: 105/10/051,307
CURRENT FILLING DATE: 2002-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION: Expressed Sequences of Arabidopsis ITLE OF INVENTION: thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.4; DB 10;
Pred. No. 1.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.4; DB 9;
Pred. No. 2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/770,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 911
SOFTWARE: FastSEQ for Windows Version 4.0
                    Application US/09770696
0010044940A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60/178,278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/263,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10051307
Patent No. US20020170095A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-696-344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AAGTTTCTTGAGGCTCC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.3%;
94.1%;
                                                                                                                                                                                                                                        ige, Amy
itthew, Abraham V
edford, Brooke L.
                                                                                                                                                                                             ı, Yang
ameaka, Joshua G
                                                                                                                             amilton, Carol M
rice, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 73.3%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-10-051-307-4
                                                                                                                                                                            Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 73.3
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             wis, Keith R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoffman, Neil
                                                                                                                                                                                                                                                                                                                                                                                                                                    llen, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin Ver.
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DAI, ZIYU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-10-051-307-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000817
CURRENT APPLICATION NUMBER: US/09/949,654
CURRENT FILING DATE: 2001-09-12
PRIOR FILING DATE: 2000-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15.8; DB 10; Length 368004; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 3072;
                                                                                                                    APPLICANT: Presc, James R.
APPLICANT: Presc, James R.
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
TITLE OF INVENTION: SOLUBLE ZALPHAIL CYTOKINE RECEPTORS
FILE REPERENCE: 00-22
CURRENT APPLICATION NUMBER: US/09/825,561A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/194,731
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score 16.2; DE Pred. No. 82; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                          Sprecher, Cindy A.
No. US20020137677Alak, Julia E.
West, James W.
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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, Application US/09825561A
US20020137677A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , LOCATION: (1)...(368004); OTHER INFORMATION: n = A,T,C or GUS-09-949-654-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09949654
Patent No. US20020127644A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 77.1%;
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (54)...(491)
US-09-825-561A-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3
LENGTH: 368004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
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ò g Gaps

Gaps

RESULT 11

q

Length 7792;

73.3%; Score 15.4; DB 12; 94.1%; Pred. No. 2.3e+02; tive 0; Mismatches 1;

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APPLICANT: Olds Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILLE REFERENCE: PA-0028 US.
CURRENT APPLICATION NUMBER: US./10/044,090
CURRENT FILLING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SSEQ ID NO 359
LENGTH: 7792
                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 2171870CB1
US-10-044-090-359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: July 9, 2003, 02:22:33 Job time: 122.338 secs
Sequence 359, Application US/10044090 Patent No. US20020137081A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5170 GAAGGTTCTTGAGGCTC 5154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 GAAGTTTCTTGAGGCTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                         APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIP1300-3
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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; Patent No. US20020123619A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Lodes, Michael J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS NO ELUNG CANCER
; FILE REFERENCE: 210121.556
; CURRENT FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 175

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Pred. No. 2.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.4; DB 9;
Pred. No. 2.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DAFE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
NUMBER OF SEQ ID NOS: 5379
LENGTH: 2979
                                                                                                                                                               Sequence 48, Application US/09938842A Patent No. US20020160378A1
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Best Local Similarity 94.1%; Pr
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   584 GAAGITICITICAGICIC 600
                          139 GAAGTTCTTGAGGCGC 155
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    GAAGTTTCTTGAGGCTC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Arabidopsis thaliana US-09-938-842A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.3%;
Best Local Similarity 94.1%;
Matches 16; Conservative
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; ORGANISM: Homo sapiens
US-09-960-253-175
                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-960-253-175/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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RESULT 15 US-10-044-090-359/c

Scoring table:

Total number

Searched:

Minimum DB s Maximum DB s

Database

Perfect score:

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Sequence:

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AW845925 416 bp mRNA linear EST 19-MAY-2000 QV4-CT0141-170999-003-e05 CT0141 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                  BH071641 RPCI-24-3
BA938634 AGENCOURT
AA960891 on9710.s
B1478067 dai0910.s
AA570749 nf21408.s
T96412 ye34e06.s1
AQ828497 HS.525_B
AQ060080 CIT-HSP-2
                                                                                                                                                                                                                                                                                                                                                                                                            AI858370 w137c06.x
AV116750 AV116750
AW418979 ha16c08.x
AI949943 wq04e12.x
AA040036 zk47f02.s
BG131509 EST464401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                     AQ060080 CIT-HSP-2
AI651188 wb05f07.x
AK015246 Mus muscu
AV713343 AV713343
BB463960 BB463960
                                               AA521007 aa70e02.s
BI065269 pgfln.pk0
BG351521 109E03 Ma
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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     A2484779
BQ994599 (
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Fax: +55-11-2707001
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319.453 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV4-CT0141-170
999-003-e05&t3=1999-09-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 45
High quality sequence.stop: 302.
                                                                                                                                                                                                                                                                                       Anotes Organ: colon; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mrNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wistow, G., Bernstein, S.L., Wyatt, M.K., Ray, S., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of human retina for the NEIBank Project: Retbindin, an abundant, novel retinal CDNA and alternative splicing of other retina-preferred gene transcripts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ636494 14man Retina CDNA (Un normalized, unamplified): hd/he Homo sapiens cDNA clone hd10d06 5', mRNA sequence.
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was dissected from two 80 year old donors with no observed
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/db_xref="taxon:9606"
/clone="hd10d06"
/clone_lib="Human Retina CDNA (Un-normalized, unamplified
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1 (bases 1 to 463)
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Pred. No: 3.2e+02;
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Plate: 10 row: a column: 06
Seq primer: MI3RPI reverse primer (ABI).
Location/Qualifiers
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                                                                                                                                                                                                            organism="Homo sapiens"
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/clone_lib="CT0141"
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Local Similarity 90.5%;
les 19; Conservative
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Fax: 301 496 0078
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eye disease. 100ug of total RNA was used for library construction. A directionally cloned CDRA library in the pspoRTI vector (Life Technologies) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are confrained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I
                                                                                                                                                                                                          primer-adapter [5'-pGACTACTTCTACATCGCGACGCGCCCCC(T)15-3']. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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BOGXG49TR BOGX Brassica oleracea genomic clone BOGXG49, DNA
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Seg primer: TR
Class: sheared ends.
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Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Wholished (2001)
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Pred. No. 6.1e+02;
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Pred. No. 3.4e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 90.5%;
Matches 19; Conservative (
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301-838-0208
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, J., Ishikawa, T., Kai, C., Kawai, J., Kikuchi, N.,
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Mammalia; Eutheria;
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55 c
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rel: 319 335 8250
Fax: 319 335 9565
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Best Local Similarity
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BB230340/c
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AUTHORS
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SOURCE
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UI-R-C2-nj-b-10-0-UI.sl UI-R-C2 Rattus norvegicus cDNA clone
UI-R-C2-nj-b-10-0-UI 3', mRNA sequence
   BH140462 11near GSS 07-AUG-2001
ZMMBBD0002F02r Maize B73 Zea mays genomic clone ZMMBBD0002F02r, DNA
                                                                                                                                                          Tracheophyta;
ceae; PACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Wector: pcUGIBAC-1; Site_1: HindIII; Site_2: NotI; For more details on library preparation, ordering clones and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /www.genome.clemson.edu/projects/stc/maize/zMMBBb
2 c 159 q 190 t
                                                                                                                                                                                                                              Tomkins,J.P., Main,D., Goicoechea,J.L., Frisch,D.A. and Wing,R.A.
A Deep-Coverage BAC Library for Maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoldeae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 17;
Pred. No. 9.6e+02;
                                                                                                                                                                                                                                                                                                                                                 SC 29634, USA
                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Young leaves"
/lab_host="E. coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone-"ZMMBBb0002F02r"
                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 619.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="Maize_B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Zea mays"
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                                                                                                                                                                                                                                                                                                                                Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                      Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'cultivar="B73"
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                                                                                GI:15099523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="B73"
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                                                                                                                                                                                                                                                                       Unpublished (2001)
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Best Local Similarity 100.
Matches 17; Conservative
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TITLE
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COMMENT
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TITLE
JOURNAL
COMMENT
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AI071748
                                                              ACCESSION
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/docto="Vector: pr730-pec (Pharmedia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C2 library is a subtracted library derived from the UI-R-C2 library, which is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C1 library, which is a subtracted library derived from the UI-R-C1 library. The UI-R-C0 library derived from the UI-R-C0 library derived from the UI-R-C0 library derived from at placenta, adult lung, brain, liver kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone within the mixture. The subtracted library of origin of a clone within the mixture as follows: PCR amplified CDNA inserts from UI-R-C1 clones from which 3' ESTS had been derived was used as a driver in a hybridization with the UI-R-C1 library in the form of single-stranded circles: The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NA linear EST 03-JUL-2000
3 days neonate thymus Mus
               The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized adult 8-Day-Embryo library. cDNA Library Preparation: M. Fatima Bonaido, Ph.D. clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A. G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE ID=1776381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     converted to double-stranded circles and electroporated thro DHIOB bacteria (Life Technologies) to generate the UI-R-C2 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
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90.0%; Pred. No. 8.5e+02;
1ve 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
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BB230340 RIKEN full-length enriched,
musculus CDNA clone A630026D12 3', mR
BB230340
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Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="Spraque-Dawley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="UI-R-C2"
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                                                                                                                                                                                                                                                                                      Seq primer: M13 Forward POLYA=No.
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.

Chordata; Rodentia;

EST 21-JUL-2000

linear

MRNA

299 bp

BB449612

RESULT 7 BB449612/c LOCUS DEFINITION

BB449612 RIKEN full-length enriched, 9 days embryo Mus musculus

CDNA clone D030072M21 3', mRNA sequence. BB449612

BB449612.1 GI:9310647

ACCESSION

Mus musculus house mouse.

SOURCE

KEYWORDS

VERSION

REFERENCE AUTHORS

```
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama.Y., Westover.A., Itoh,M., Nagaoka.S., Sasaki.
N., Okazaki.Y., Muramatsu,M. and Hayashizaki.Y.
Therimostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Rawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shipanto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
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modified pBluescript KS(+) after bulk excision from Lambda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primed with a primer [5' GAGAGAGGAGAAGAGACCTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(58C), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/organtsm="Mus musculus"
/db_xref="taxon:10090"
/clone="A630026612"
                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
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| (bases i to 299) | Konnoh H. Alzawa, K. Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Erkunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Kal, T., Kal, T., Kal, T., Kal, M., Kaloda, K., Kagawa, T., Kal, C., Kawal, J., Kikuchi, N., Kiyosawa, H., Kolima, Y., Kondo, S., Koya, S., Kurihara, C., Rusakabe, M. Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Salto, H., Sakai, C., Sato, K., Shibata, X., Shibata, Y., Shipane, Y., Shibaya, A., Shiraki, T., Soqabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Fakahashi, F., Tominaga, N., Toya, T. Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic

RIKEN Mouse ESTS (Konno, H., et al.) Unpublished (2000)

TITLE JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998).
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contributed to prepare mouse tissues. 1st strand cDNA was
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was cleaved with BamHI and XhoI. Vector: a modified
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/lab_host="DH108"
                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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Gaps

Length 250; Indels

Score 16.8; DB 10; Pred. No. 8.5e+02;

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Query Match Best Local Similarity Matches 18; Conserv

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Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Ragwa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
, Y., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
Yano, R., Yasuhishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
, M., Muramatsu, M. and Hayashizaki, Y.
FIKEN Wouse ESTS (Konno, H., et al.)
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URL.http://genome.gsc.riken.go.jp,
Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
A., Okazaki,Y., Muramataya.M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Ttoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                            BB548769 RIKEN full-length enriched, 2 days pregnant adult female oviduct Mus musculus cDNA clone E230012D10 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sciences Center(GSC), Tokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
after bulk excision from Lambda FLC I."
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clone_llb="RIKEN full-length enriched, 2 days pregnant
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Carninci,P. and Hayashizaki,Y.
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                                                                                                          Length 299;
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                                                                                                            Score 16.8; DB 10;
Pred. No. 9e+02;
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                                                                                                            Query Match 80.0%;
Best Local Similarity 90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E.,
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                                                                                                                                                                                                                                                                                                                                                                                         Length 305;
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); Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 0311 row: C column: 02
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erron
Plate: 0311 row: C column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 471. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="UUGC1M0311C02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 CCCGAAGTTACTTGAGGTTC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCCGAAGITICITGAGGCIC: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:10649953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                       80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 471)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ484779.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84112,
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with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampitallin resistance."
                                                was hydrodynamically sheared by repeated passage through, a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                           10.5 kb range using preparative agarse gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGF7K21.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone GGF7K21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kozik, A. Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Zlegle, J., Ellison
P., Kolkman, J., Slabaugh, M.S., Litvingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBRcDNASflAB; The library was constructed from 10 different sources.of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: akozikéatgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig5566, see http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0; .Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 17; Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="QG_EFGHJ lettuce serriola"
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8; DB 1
Pred. No. 1e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://compgenomics.ucdavis.edu/
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Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.08;
ilarity 90.08;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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KEYWORDS
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οy a

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This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com High quality sequence stop: 406.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF070228 557 bp mRNA linear EST 06-DEC-2001 st08f11.yl Gm-c1065'Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1065-742 5' similar to TR:Q92QA1 Q92QA1 F13K3.13 PROTEIN: ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A. (Joses, I. W. 1971). Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Myller, T., Underwood, K., Stepfoce, M., Thelsing, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                       directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptophyta; Embryophyta; Tracheophyta;
                                                                                                               construction can be obtained at http://cgpdb.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBlueScript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being
source of RNA. cDNAs were then pooled, size-fractionated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cold stressed for 2 days at 4C. Complementary DNA wasynthesized from mRNA using a primer consisting of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tragments were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/clone_lib="Gm-c1065"
                                                                                                                                                                                                                                                                                                              Length 548;
                                                                                                                                                                                                                         ·1 others
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                                                                                                                                       TAG_LIB=OG_EFGHJ lettuce serriola
TAG_TISSUE-flowers environmental stress
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                                                                                                                                                                                                                                                                                                        80.0%; Score 16.8; DB 14;
90.0%; Pred. No. 1.1e+03;
ative 0; Mismatches 2;
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/lab_host="DH108"
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                                                                                                                                                                                           TAG_SEQ-CGAATGCGGG"
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                                                                                                                                                                                                                               148 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson:wustl.edu
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1 (bases 1 to 567)
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88
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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directionally cloned into the EcoRI-XhoI restriction

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1 CCCGAAGTTTCTTGAGGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
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                                                                                                                                                                                                                                                                                                Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG351521
BG351521.1
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ses 18; Conserv
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of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                  AA521007 579 bp mRNA linear EST 20-AUG-1997 aa70e02 sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826298 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 579)
NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                               Length 567;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ph.D., Gerald Marti, M.D. cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                            1 others
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tissue_type="germinal center B cell"
                                                                                                                               Score 16.8; DB 12;
Pred. No. 1.1e+03;
0; Mismatches 2;
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Pred. No. 1.1e+03;
0; Mismatches 2;
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 146.
Location/Qualifiers
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'clone="IMAGE:826298"
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90.08;
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1 Similarity 90.0%;
18; Conservative
                                                         Shoemaker.
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Best Local Similarity 90.0
Matches 18; Conservative
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Best Local Similarity
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pq: pgfin.pk004.bll.normalized chicken fat cDNA library Gallus gallus cDNA clone pgfin.pk004.bll 5' similar to no significant hits (plog(P) 4)G, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
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109E03 Mature tuber lambda ZAP Solanum tuberosum CDNA, mRNA
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/clone_lib="normalized chicken fat cDNA library"
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
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Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E.coli EMDH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male and Female"
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161 c 175 q
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Nielsen, K. L, Crookshanks, M.
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Institut for bioteknologi
                                          388 CCCGGAGTTTCTTGAAGCTC 407
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Larry A. Cogburn
University of Delaware
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90.0%;
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Search completed: July
Job time: 1069.8 secs
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Clifton, S., Johnson, S. L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW148283 1705 bp mRNA linear EST 22-JUN-200 dalth03.x1 normalized Xenopus laevis gastrula Xenopus laevis cDNA clone XENOPUS_SOURCE_ID:x1nga001h06 3' similar to SW:TPR_HUMAN P12270 NUCLEOPROTEIN TPR. [1] ;, mRNA sequence.
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Xho1; cDNA was prepared from 2ug of poly A+ RNA (equal
parts from stage 10.5 and stage 11.5 gastrulae).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
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clone_lib="normalized Xenopus laevis gastrula"
'tissue_type="gastrula (stages 10.5, 11.5 mixed)"
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16.8; DB 12; Length 684;
Pred. No. 1.2e+03;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                /clone_lib="Mature tuber lambda ZAP"
/tissue_type="Tuber"
/note="Vector: Lambda ZAP"
129 c 167 g 197 t
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Washington University School of Medicine
                                                                                                                                                                                            /organism="Solanum tuberosum"
/cultivar="Field grown Kuras"
/db_xref="taxon:4113"
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Library normalized by Jihwan Song
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Seg primer: -400P from Glbco
High quality sequence stop: 476.
Location/Qualiflers
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Unpublished (1999)
                                           Email: kgw@bio.auc.dk
Sequenced from the 5' end.
High quality sequence stop: 684
POLYA-No.
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                                                                                                                                                 Location/Qualifiers
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ilarity 90.0%;
Conservative C
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Tel: +45 96358467
                         Fax: +45 98141808
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Matches 18; Conserv
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ECORI-XhoI cut cDNA was then ligated into Unizap-XR (Stratagene) with ECORI at the 5' end and XhoI at the 3' end .S-library phagemids were prepared by mass excision from the original library and normalized by hybridization to biotinylated driver (prepared from the same library by PCR) to Cot-onega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Cho et al. 1991 Cell 67, 1111-1120). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished). Note: This is a Xenopus Gene Collection (XGC) library.

ARSE COUNT 148 a 139 c 192 g 223 t 3 others

RRIGIN 80.0%; Score 16.8; DB 10; Length 705;

Best Local Similarity 90.0%; Pred. No. 1.2e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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OM nucleic - nucleic	c search, using sw model		
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Pred. No. is the number of results predicted by chance to have a

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Rabsbroks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,

Benton,J., Blumage,R., Blankenburg,K., Bonnin,D., Bouck,J.,

Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,

Burch,P., Burkett,C., Burrell,K.L., Byrad,N.C., Carron,T.F.,

Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Coyle,M.D., Dathorne,S.R., David,R., Davlla,M.L., Davis,C.C.,

Coyle,M.D., Dathorne,S.R., David,R., Davila,M., Davis,C.D.,

Davy-Carroll,L., Dederich,D.A., Delahaey, K.R., Deladao,S.,

Davy-Carroll,L., Dederich,D.A., Delahaey, K.R., Deladao,O.,

Dugan-Rocha,S., Durbin,R.J., Earnhart,C., Edgap,N., Erader,C.,

Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,

Roster,P., Frantz,P., Gabis,A., Gao,J., Garcia,A., Ganner,T.,

Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S.,

Hamilton,K., Harris,C., Harris,K., Hart,M., Hallak,P., Hawes,A.,

Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,

Joudah,S., Karlsson,E., Relly,S., Khan,U., King,L., Korvah,J.,

Loulseqed,H., Lozado,R.J., Lu,X., Lucier,N., Lucier,R., Luna,R.,

Loulseqed,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R.,

Loulseqed,H., Lozado,R.J., Mapua,P., Martindale,R.,

May,J., Mapua,P., Martin, R., Martindale,R.,

May,J., Mapua,P., Martin, R., Martindale,R.,

Loulseqed,H., Lozado,R.J., Lu,X., Lucier,R., Lucier,R.,

May,J., Mapua,P., Martin,M., R., Lude,R.,

May,J., Mapua,P., Martin,M., Lude,R.,

May,J., Mapua,P., Martin,M., Lude,R.,

May,J., Mapua,P., Martin,M., Rude,R.,

May,J., Martin,M., R., Martin,M., Lude,R.,

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May,J., Martinda,R., Martin,M., Lude,R.,

May,J., Martin,M., R., Martin,M., Lude,R.,

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Rattus norvegicus clone CH230-516, *** SEQUENCING IN PROGRESS ***,
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Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.
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lei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.
lorgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
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On Dec 20, 2001 this sequence version replaced gi:15624568.
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all,R., Wang,S., Ward-Moore,S., Warren,F
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Mammalla; Eutheria; Rodentia;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schwartz,J.C., Gros,C., Oulmet,T., Rose,C., Bonhomme,M.C. and Schwartz,J.C., Gros,C., Oulmet,T., Rose,C., Bonhomme,M.C. and Facchinetil.P.
Novel nep 11 membrane metalloprotease and its use for screening inhibitors useful in therapy
Patent: WO 9953077-A 1 21-027-1999;
INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); GUINET TANJA (FR); ROSE CHRISTIANE (FR); BONHOWME MARIE CHAMMAL (FR); BACKHINETI PATRICIA (FR)
                                  (FR); GROS
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Patent: WO 9953077-A 19 21-OCT-1999;
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CLAUDE (FR); COUIMET TANJA (FR); ROSE CHRISTIANE (FR);
MARIE CHAWALL (FR); FACCHINETTI PATRICIA (FR)
Location/Qualifiers
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/db_xref="taxon:10117"
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., Villalon, D., Vinson, R.

Shooshtari, N.

Shen, H

Scott, G.,

, Nickerson, E., Nwokenkwo, S

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Ouery Match : 100.0%; Score 19; DB 2; Length 174953; Best Local Similarity 100.0%; Pred. No. 13; Matches 19; Conservative 0; Mismatches 0; Indels 0;
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                                                                        Consensus quality: 152255 bases at least Q40 Consensus quality: 158448 bases at least Q30 Consensus quality: 164461 bases at least Q30 Estimated insert size: 155965; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Center clone name: CH230-516
------ Summary Statistics
Assembly program: Phrap; version 0.990329First call
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Kobe University
6500017, Japan
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Ikeda, K.,
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                                                                                                                                                                                                                                                                                                                                                               Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                    Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most trapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases J. Biol. Chem. 276 (24), 21895-21901 (2001)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostoml,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 2601)
complete cds.
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Sinctani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
Maruyama, K., Kiryu Seo, S., Kiyama, H., Iwata, H., Tomita, T.,
Iwatsubo, T. and Saido, T.C.
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Mus musculus neprilysin-like peptidase alpha mRNA,
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Pred. No. 1.5e+02;
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/organ1sm="Mus musculus"
/db_xref="taxon:10090"
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AF157106
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AF302076 2652 bp mRNA linear ROD 11-JUN-2001
Mus musculus neprilysin-like peptidase beta mRNA, complete cds.
AF302076
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AQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPWKRCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGY PDY I LEDNNKHLDEEY SSLTFY EDLY FENGLONLK
                                                  membrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a variety of vasoactive peptides 2011457 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SEP(delta); metalloprotease; alternatively spliced"
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                                                                                                                                                                                                                                                                                                                       itted (08-JUN-1999) International Center for Medical Research,
University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
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Sciurognathi; Muridae; Murinae; Mus.
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Emoto, N., Raharjo, S.B., Nurhantari, Y., Saiki, K.,
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Pred. No. 1.5e+02;
0; Mismatches 1;
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/db_xref="G1:6467401"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"/db_xref="taxon:10090"
                                                                                                                                                                                                                                                            Ikeda,K., Emoto,N. and Matsuo,M. Direct Submission
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 2652)
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Shirotani, K. and Saido, T.C.
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                                         Yokoyama, M. and Matsuo, M.
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Best Local Similarity 94.7
Matches 18; Conservative
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DQNLSKESAMVREEMAEVLELETHLANATVPQEKRHDVTALYHRMDLMELQERFGLKG
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FSARHFQQQSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNGGVRQAYKAYLRWLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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Direct Submission
Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
                                                                                                                                                                                                                                                                                                                          /translation="MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIGKQI
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Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases
J. Blol. Chem. 276 (24), 21895-21901 (2001)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2694)
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peptidase gamma mRNA, complete cds
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                                                                                                                                                                                                                                                     /product="neprilysin-like peptidase beta"
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Pred. No. 1.5e+02;
; Mismatches 1;
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                                                                                                                                                                                                                                                                          /protein_id="AAG18447.1"
/db_xref="GI:10505362"
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/db_xref="taxon:10090"
25. .2364
                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                          /note="endopeptidase"
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Mus musculus neprilysin-like |
AF302077
                                                                                          Location/Qualifiers
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Best Local Similarity 94.7%;
Matches 18; Conservative
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AF157105. 2892 bp mRNA linear ROD 25-NOV-1999
Mus musculus soluble secreted endopeptidase mRNA, complete cds.
AF157105
                                                                     /translation-"MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIALRD
SSLKSDICTTPECVIAAARILENMDQSRNPCENFYQYACGGWLRHHVIPETNSRYSVF
DILRDELEVILKGVLEDSTSGHRAPRAKTLYRSCMNGSVIEKRDSEPLLSVLKWVG
GWPVAADRWNFTMGLKRELERQIAVLNSOFNRRVLIDLFIWNDDONSSRYIYIIDOP
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GAAVVNAFYSPNRNQIVFPAGILQPPFFSKDQPQSLNFGGIGMYIGHEITHGFDDNGR
NFDKNGNMLDWWSNFSARHFQQOSQCMIYQYGNFSWELADNQNVNGFSTLGENIADNG
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FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
                                                                                                                                                                       LGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRKDQNLSKESAMVREEMAEVLELET
HLANATVPQEKRHDVTALYHRMDLMELQERFGLKDRVSLCSPGCPGTHSVDQAGLELG
                                                                                                                                                                                                                        NPPASDSRVLGLKGFNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSA
RTWQNYLVWRLVLDRIGSLSQRFKEARVDYRKALYGTTVVEEVRWRECVSYVNSNWESA
                                                                                                                                                                                                                                                                                                                                                                       GVRQAYKAYLRWLADGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDV
HSPLKYRVLGSLQNLPGFSEAFHCPRGSPMHPWKRCRIW"
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Submitted (08-JUN-1999) International Center for Medical Reseas
Kobe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2694;
'product="neprilysin-like peptidase gamma"
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/protein_id="AAF13152.1"
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Pred. No. 1.5e+02;
0; Mismatches 1;
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/note="SEP; metalloprotease"
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Yokoyama,M. and Matsuo,M.
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1 Similarity 94.7%;
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Mus musculus
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FSAHHFQQOSQCMIYQTGNFSWELADNQNYNGFSSLGENIADNGGYRQAYKAYLRWLA
DGGKDQRLPGLNLTYAQLFFINYAQVWGGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
LPGFSEBAPHPMKRCHW"
774 c 827 g 574 t
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Patent: WO 0047750-A 12 17-AUG-2000;
BOILEAU GUY (CA) ; DESGROSEILLERS LUC (CA) ; UNIVERSTIE DE MONTREAL
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DGGKDQRLPGLNLTYAQLFFINYAQVWCGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
RIGSLSORFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
                                DEEY SSLTFY EDLY FENGLONLK NNAORSLKKLREKVDONLWI IGAAVV NAFY SPNRN
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Mammalia, Eutheria, Rodentia, Sclurognathi, Muridae, Murinae, Mus
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Pred. No. 1.5e+02;
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Pred. No. 1.5e+02;
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'note="unnamed protein product"
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Sequence 12 from Patent WO0047750.
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Boileau, G. and Desgroseillers, L.
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RESULT 10 AF176569

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AF176569 2925 bp mRNA linear ROD 11-MAY-2000
Mus musculus neprilysin-like metallopeptidase l (N11) mRNA,
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DGGKDQRLFGLNLTYAQLFFINYAQVWGGSYRPEFAVQSIKTDVHSPLKYRVLGSLQN
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RP23-15L19, *** SEQUENCING IN
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                              Seidah, N.G., Crine, P., Desgroseillers, L. and Boileau, G. Molecular clothing and blochemical characterization of a new metestis soluble-zinc-metallopeptidase of the neprilysin family Biochem. J. 347 (Pt. 2), 419-429 (2000)
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Mus musculus
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Ghaddar,G., Ruchon,A.F., Carpentier,M., Marcinklewicz,M.,
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Ghaddar, G.; Ruchon, A.F., DesGroseillers, L. and Boileau, G.
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Submitted (09-A010-1999) Biochemistry, University
Edouard Montperit, Montreal, Que H3T 134, Canada
Location/Qualifiers
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Pred. No. 1.5e+02;
0; Mismatches 1;
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/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="testis"
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Mus musculus chromosome 4 clone R
PROGRESS ***, 2 unordered pieces.
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Best Local Similarity 94.7%;
Matches 18; Conservative
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/gene="N11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL607032.15
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Submitted (23-50N-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Jun 23, 2002 this sequence version replaced gi:21105067.
                                                                                                                                                                                                                                                                                Genome Sequencing Center, 4444 Forest Park
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 9.21 in Q20 bases; agarose-fp
Quality coverage: 9.27 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 74317 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 26801 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of unknown length
contig of 4084 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 3907 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 133 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 229530 bases at least 040 Consensus quality: 230520 bases at least 030 Consensus quality: 231021 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 216000; agarose-fp
Insert size: 233756; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project Information
                                                                                                                                   McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                 Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 233488)
McPherson, J. D. and Waterston, R. H.
                                                                                                                                                                                                                           McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: submissions@watson.wustl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: M_BA0131N12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Center
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                                                                                                                                                                                                                                                                           Submitted (23-MAY-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13;
                                                                                                                                                                                                       (bases 1 to 233488)
                                                                                                                (bases 1 to 233488)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
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Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                        Direct Submission
Submitted (23-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                            Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terninator; 11% of reads Chemistry: Dye-terninator; 11% of reads Chemistry: Dye-terminator Big Dye; 80% of reads Consensus quality: 207834 bases at least 040 Consensus quality: 207956 bases at least 030 Consensus quality: 208060 bases at least 020 Insert size: 208149; sum-of-contigs at least 020 Insert size: 219051; 2.3% error; agarose-fp Quality coverage: 12.41x in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                         Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC122228.2 GI:21539800
HTG; HTGS_PHASE1; HTGS_FULLTOP
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Pred. No. 98;
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53647 c 51328 g 49076 t
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                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                              Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db_xref="taxon:10090"
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1 Similarity 94.7%;
18; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 19336)
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Bakkeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Ho, S.-L., idol, J. R., Karlins, E., Laric, P., Lee-Lin, S.-Q.,
Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Maskeri, B.,
Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A.
Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (21-FEB-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Galthersburg, MD 20877, USA
3 (bases 1 to 193363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-FEB-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Feb 20, 2002 this sequence version replaced gi:13027532.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data in this record represents an 'enhanced' version of a phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair
                                                                                                                                                                                                                                                                                                                     Length 233488;
                                                                                                                                                                                                                                               600 others
                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: NIH Intramural Sequencing Center
                                                                                           109510. .233032.
/note="assembly_name:Contig85"
233133. .233265.
/note="assembly_name:Contig18"
23336. .233488
/note="assembly_name:Contig19"
a 57044 c 53747 g 59136 t 6
                                                                                                                                                                                                                                                                                                                        Score 17; DB 2; L. Pred. No. 1.6e+02;
                                              note="assembly_name:Cont1g83"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: nisc_mouse@nhgrl.nih.gov
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: qn
Center clone name: 454P08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE2; HTGS_DRAFT.
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27604 TCGGCTACCCTGACTAC 27588
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                                                                                                                                                                                                                                                                                                                                                                                                                           3 TCGGCTACCCTGACTAC 19
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.34992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             musculus.
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Best Local Similarity
Matches 17; Conserva
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                                                                                                                                                                                                                                                 .62961
misc_feature
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data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g. human), and/or confirmation by PCR testing. In addition,

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(center project name ye)'
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note="clone overlaps with GenBank Accession Number
CO90443 clone RP23-434H17 (center project name qm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenBank Accession Number
the sequence assembly is based on at least.8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base'ls associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                Insert size: 192763; sum-of-contigs
Quality coverage: 13.44x in Q20 bases; agarose-fp
Quality coverage: 11.17x in Q20 bases; pulse-field-ge.
Quality coverage: 11.17x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                      Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 192013 bases at least Q40 Consensus quality: 192474 bases at least Q30 Consensus quality: 192660 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                number will be preserved.
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of 29384 bp in length
unknown length
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unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP23-454P8"
/clone_lib="RPCI mouse BAC library 23"
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                                                                                                                                                                                                                                                                                                          Insert size: 179000; agarose-fp
Insert size: 209000; pulse-field
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168922. 193363
/note="clone overlaps with
AC026478 clone RP23-135F23
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                                                                                              with a Phrap-derived quality score.
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note="assembly_fragment"
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/note="assembly_fragment"
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note="assembly_fragment"
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LOCUS
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                                                                                                                                                                                                                                                                         HTG 25-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 204867)
McPherson, J. D. and Waterston, R. H.
The sequence of Mus musculus clone
                                                                                                       Gaps
                                                                                                                                                                                                                                                     MUS MUSCULUS Chromosome UNK clone RP23-225D14, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as
                                                                  Length 193363;
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         601 other's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5227: contig of 5227 bp in length
5327: gap of unknown length
28642: contig of 23315 bp in length
28742: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 136000; agarose-fp
Insert size: 205765; sum-of-contigs
Quality coverage: 12.50 in Q20 bases; agarose-fp
Quality coverage: 12.91 in Q20 bases; sum-of-conf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index:shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version 0.990319
Consensus quality: 203471 bases at least Q40
Consensus quality: 203858 bases at least Q30
Consensus quality: 203980 bases at least Q30
                                                              4; DB 2;
3.5e+02;
42427 c 41080 g 52049 t
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                                                                                                 Mismatches
                                                              Score 16.4;
Pred. No. 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 204867)
McPherson, J.D. and Waterston, R.H..
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 204867) McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: M_BA0225D14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Center
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                          160167 GATCGCTACCTGACTA 160150
                                                                                                                                    1 GATCGGCTACCCTGACTA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13;
                                                          86.3%;
llarity 94.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28642:
28742:
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Best Local Similarity
Matches · 17; Conserv
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AC121567
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   BASE COUNT
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AUTHORS
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AC115760 206132 bp DNA linear HTG 26-JUN-2002
Mus musculus clone RP23-62M14, WORKING DRAFT SEQUENCE, 18 ordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R. Severy, P., Spencer, B., Stange Thomann, N., Stojanovic, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strauss, N., Subramanian, A., Talamas, J.; Tesfaye, S., Theodore, J. Tophan, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wiman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J. Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.4; DB 2; Length 204867;
Pred. No. 3.5e+02;
0; Mismatches 1; Indels 0;
contig of 75328 bp in length gap of unknown length contig of 100697 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-62M14
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                             ...5227
'note="assembly_name:Contig5'
                                                                                                                                                                   /organism-"Mus musculus
                                                                                                                                                                                              /db_xref="taxon:10090"
/chromosome="UNK"
                                                                                                                                                                                                                                                              /clone="RP23-225D14"
                                                                                                     Location/Qualifiers
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94.4%;
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                                                                                                                                 1. .204867
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contig of 2557 bp in length

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2 ATCGGCTACCCTGACTAC 19
                                                                                        98013
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Pheodore,J., Topham,K., Travers,M., Travis,N., Trigillo,J.,
Assillev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Coung,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (26-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                   Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W.; Illev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.
Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K.
                                                                                                                                                                         Llu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrin,J.,
Meneus,L., Mihova,T., Mleng,V., Murphy,T., Naylor,J., Nguyen,C.,
Micol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
                                                                                                                                                                                                                                                                                       O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rösetti, M., Koy, A., Santos, R., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schaus, S., Severy, P., Spencer, B., Stange-Thomann, N. Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     believed to be correct as given, however the sizes
the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 26, 2002 this sequence version replaced g1:19683412
All repeats were identified using RepeatMasker:
., Cooke,P., DeArellano,K.; Dewar,K., Diaz,J.S., Dod
., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are represented as runs of N. The order of the pleces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 204432; sum-of-contigs
Quality coverage: 7.1 in Q20 bases; agarose-fp
Quality coverage: 7.3 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Summary Statistics vector: Plasmid; n/a; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 199666 bases at least 040 Consensus quality: 202898 bases at least 030 Consensus quality: 203843 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3891 3990: gap of 100 bp
3991 80283: contig of 76293 bp in length
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1 3890: contig of 3890 bp in length
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contig of 1689 bp in length
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contig of 1893 bp in length
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contig of 1300 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             his sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone name: 62_M_14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  provided by the submittor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name:
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168 bp in length
            bp in length
                                                  97912: contig of 1753 bp in length
                                                                                        contig of 1885 bp in length
                                                                                                                                                                                                                                                                                                             1 206132: contig of 282 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 86.3%; Score 16.4; DB 2;
Best Local Similarity 94.4%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 1;
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44062 c. 44541 g 57492 t
            contig of 2467
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note="assembly_fragment"
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750: contig of 77
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8 83.2 2262 22 8 83.2 2318 24	15.8 83.2 2540 23 ABL22299 15.8 83.2 2580 24 ABN84280	8 83.2 2636 22 AAF59660 8 83.2 2663 22 AAF59661	17 15.8 83.2 2676 21 AAA63764 18 15.8 83.2 2714 22 AAF59659 19 15.8 83.2 2893 24 ABN84279	20 15.8 83.2 2893 24 AAD28544 c 21 15.8 83.2 2928 23 AAS73816	22 15.8 83.2 2953 24 23 15.8 83.2 2975 24 24 15.8 63.2 5120 23	8 83.2 2012 2 ABL22310 8 83.2 30510 22 ABA15643	15.4 81.1 351 22 AA190/46	29 15.4 81.1 574 24 ABL49463 30 15.4 81.1 574 24 ABK30650 31 15.4 81.1 565 31 NACASTO	15.4 81.1 676 22 AAF61318 15.4 81.1 676 22 AAF61318	34 15.4 81.1 967 24 ABN98526 Are	14.8 77.9 306 24 ABL75107	38 14.8 77.9 2635 23 ABL20713	14.8 77.9 5250 22 AAS2921 14.8 77.9 5250 22 AAL0553 14 8 77 9 5276 23 ARIO671	14.8 77.9 7397 23 ABL11030	14.4 75.8 337 24 ABN21293 14.4 75.8 1737 23 ABL13229		ALIGNMENTS		AA228825 ID AA228825 standard; DNA; 19 BP.	XX AC AA228025;	DT 01-FEB-2000 (first entry)		KW Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation, KW neuron; hormone; peptide messenger; inhibitor; detection; disorder, KW cardiovascular disease; neurodegenerative disease; growth disorder, KW hynothalamic-hynophysea] axis; endortine disorder: brobe; hybridsal	XX XX OS Synthetic.	XX PN FR2777291-A1.	XX PD 15-OCT-1999. XX		PR 08-APR-1998; 98FR-0004389. XX	sed to PA (INRM) 1 y neut XX novel PI Outmet T,	ing novel PI Schwartz JC; s Sequenc XX WP: 1999-593429/51	
GenCore version 5.1.6	(c) 1993 - 2003	OM nucleic - nucleic search, using sw model	Run on: July 8, 2003, 00:43:28 ; Search time 119.376 Seconds (without alignments) 358.431 Million cell updates/sec	US-09-647-780A-19	erfect score: 19 equence: i gatcggctaccctgactac 19	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 2185239 seqs, 1125999159 residues	Total number of hits satisfying chosen parameters: 4370478	Minimum DB seq length: 0 Maximum DB seq length: 200000000	minim . Minim	Maximum Match Listing first	£	Database : N_Geneseq_101002:* 1: /SIDSZ/gogdata/geneseq/geneseqn-embl/NA1980.DAT:* . 2: /SIDSZ/gogdata/geneseq/geneseqn-embl/NA1981 nam.*	 /SIDSZ/gcgdata/yeneseq/geneseqn-emb1/NA1982.DAT:* /SIDSZ/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:* /SIDSZ/gcdata/reneseq/geneseqn-emb1/NA1983.DAT:* 	5: /SIDS2/gcgdata/geneseg/genesegn-embl/NA1984.DAT:* 6: /SIDS2/gcgdata/geneseg/genesegn-embl/NA1985.DAT:*	7: /SIDS2/gcgdata/geneseg/genesegn-embl/NA1986.DAT:*	/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988 : /SIDS2/gcgdata/geneseq/geneseqn-embl/NA198	11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:* 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*	: /SIDS2/gcgdata/ : /SIDS2/gcgdata/	: /SIDS2/ : /SIDS2/	/SIDS2/gcgdata/ /SIDS2/gcgdata/ /SIDS2/gcgdata/	. /SIDSZ/gcgdata/geneseg. . /SIDSZ/gcgdata/geneseg.	/gcgdata/geneseq/ /gcgdata/geneseq/ /gcgdata/geneseq/ /gcgdata/geneseq/	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No Score Match Length DR ID Description	19 100.0 19 20 AAZ28825	19 100.0 2286 24 AAD28130 Solv 19 100.0 2765 20 AAZ28810 Rat	.4 91.6 29 21 AAA63760 PCR prime .4 91.6 2925 21 AAA63763 CDNA enco .8 83.2 1422 23 AAS73814 DNA encod	15.8 83.2 1497 23 AAS69914 DNA encodin 15.8 83.2 2076 22 AAF89937 Nucleotide 15.8 83.2 2073 24 AAS897186 Himan meral	

Disclosure; Fig 6; 167pp; English.

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membrane metalloprotease designated neprilysine II (NRPI) gene (AA228810). NEPII is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic- hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme; gynaecological; antisense-therapy; male erectile dysfunction; MED; female sexual dysfunction; FSD; female sexual arousal disorder;
                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                           Sequences AAZ28811-Z28827 represent probes for detecting the rat
             involved in proteolysis of
to screen for inhibitors,
cardiovascular disease
                                                                                                                                                                                                                                                                                                                      Length 19;
                                                                                                                                                                                                                                                                                                                                                     Indels
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1664..2286
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/note- "Encodes catalytic domain"
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                                                                                                                                                                                                                                                                                                                    Score 19; DB 20;
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                      Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
             New membrane metalloprotease NEP II, neuronal and hormonal peptides, used potentially useful for treating e.g.
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                                                                             Claim 3; Page 24; 29pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted endopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  female sexual arousal disorder
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                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PFIZ ) PFIZER LTD.
(PFIZ ) PFIZER INC.
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Rattus sp.
                                                                                                                                                                                                                                                        disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the gene for the rat membrane metalloprotease designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidegic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or
                                                                                                                              The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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to screen for inhibitors,
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Pred. No., 2.8;
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Best Local Similarity 100.
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-1998;
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\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\ci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endocrine disorders

SC;

NEP-like enzyme; protein production; protein secretion; neurological disease; Alzheimer's disease; pain; psychiatric disorder; fertility; bone disease; abnormal phosphate metabolism; ss.

neurological

sp.

Mus

Neprilysin; neutral endopeptidase metallopeptidase-like enzyme

DNA encoding neutral endopeptidase metallopeptidase-like enzyme NL-1

(first entry)

04-DEC-2000

AAA63763;

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AAA63763 standard; cDNA; 2925 BP.

AAA63763 RESULT

/product "neutral endopeptidase metallopeptidase-like

enzyme NL-1"

Location/Qualifiers

332..2629

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PCR primers AAA63759-60 were used to amplify a murine cDNA sequence encoding a neutral endopeptidase metallopeptidase (NEP)-like polypeptide, designated NL-1. The specification also describes NL-2 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimeric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain, and psychiatric disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related
                                                                                                                                                                                                                                                                                                                                                                                              Neprilysin; neutral endopeptidase metallopeptidase-like enzyme;
NEP-like enzyme; protein production; protein secretion;
neurological disease; Alzheimer's disease; pain; psychiatric disorder;
fertility; bone disease; abnormal phosphate metabolism; PCR primer; ss
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel neutral endopeptidase-like metallopeptidase polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
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                                                      100.0%; Score 19; DB 20; Length 2765; 100.0%; Pred. No. 2.8;
                                                                                             Indels
XX
SQ. Sequence 2765 BP; 684 A; 735 C; 787 G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                             PCR primer used to amplify cDNA encoding murine NL-1.
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                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 14; 59pp; English.
                                                                                                                                               1612 GATCGGCTACCTGACTAC 1630
                                                         100.08; Pr.
                                                                                                                           1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99CA-2260376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-2000; 2000WO-CA00147
                                                                                                                                                                                                                                   AAA63760/c
ID AAA63760 standard; DNA; 29
                                                                                                                                                                                                                                                                                                                           (first_entry)
                                                                                           Conservative
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                                                                      Local Similarity
es 19; Conserv
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                                                                                                                                                                                                                                                                                        AAA63760;
                                                        Query Match
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                                                                          Best Loc
Matches
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Desgroseillers L, Boileau G;

WPI; 2000-549148/50.

P-PSDB; AAB08130

UYMO-) UNIV MONTREAL.

11-FEB-2000; 2000WO-CA00147

40200047750-A2.

17-AUG-2000.

99CA-2260376

11-FEB-1999;

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The present sequence encodes a murine neutral endopeptidase metallopeptidase-like enzyme, designated NL-1. The specification also describes NL-2 and NL-3. The NL enzymes are used to test for specific inhibitors. The N-terminal region of the enzymes can be used to promote production and secretion of foreign proteins and active biopeptides, using chimaric constructs containing the foreign protein downstream from and in phase with the N-terminal region. The NL enzymes are have been localised to the brain, and may be useful in the treatment of neurological diseases such as Alzheimer's disease, pain, targament of clasorders. NL enzymes have also been localised to the testis and ovaries, and may be used to control fertility. They have also been localised to bones, and may be used to treat bone diseases, and abnormal phosphate metabolisms related to improper peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel neutral endopeptidase-like metallopeptidase polypeptides and polynucleotides, used to screen for related sequences and enzyme inhibitors, used for the treatment of NL-3 related bone disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17.4; DB 21; Length 2925;
Pred. No. 19;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2925 BP; 710 A; 797 C; 836 G; 582 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1810 GATTGGCTACCCTGACTAC 1828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3; 59pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the NL-3 enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.68;
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Matches
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RESULT

Gaps.

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Score 17.4; DB 21; Length 29; Pred. No. 15; 0; Mismatches 1; Indels

Query Match 91.6%; Best Local Similarity 94.7%; Matches 18; Conservative

GATCGGCTACCCTGACTAC 19 29 GATTGGCTACCCTGACTAC 11

ô g

AAS73814;

11-OCT-2001

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polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II), (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                       Human, chromosome mapping, gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid sequences, AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not appear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1497 BP; 453 A; 308 C; 363 G; 373 T; 0 other;
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Pred. No. 1.2e+02;
                                                                                                                                                                                  DNA encoding novel human diagnostic protein #5718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                              13-FEB-2002 (first entry)
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Matches 17; Conservative
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P-PSDB; ABG05727.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-OCT-2001.
                                         AAS69914;
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AAF89737
ID AAF89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in responsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human DNA and
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from WIPO
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                                                                                                                                                                                                                                                                                                                                   Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Pred. No. 1.2e+02;
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Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly
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                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #9618.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 9618; 103pp; English.
AAS73814/c
ID AAS73814 standard; cDNA; 1422 BP
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Local Similarity 89.5%;
Nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217, 23-AUG-2000; 2000US-0649167,
                                                                                                                                                                                      13-FEB-2002. (first entry)
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Gaps

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AAF89737;

AAS69914/c ID AAS69914 standard; cDNA; 1497 BP

RESULT 7

22

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Query Match

Best Loc Matches

Length 1497; Indels us-09-647-780a-19.rng

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23-JUL-2001 (first entry)
                                                 19-NOV-1999;
31-MAY-2000;
31-MAY-2000;
                             Homo sapiens
                                               19-NOV-1999;
                                          25-MAY-2001
                          Gilles
                                Key
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immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.

Score 15.8; DB 24; Length 2232;

83.28;

Query Match

DB 22;

Score 15.8;

83.2%;

Query Match

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                                                                                                                                                  angina pectoris; myocardial infarction; stroke, ulcer; allergy, benign prostatic hypertrophy; migraine; psychotic disorder; benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple sclerosis; Alzheimer's disease; neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm; subarachnoid hemorrhage; cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Immune disorder, arthritis, endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia, Huntington's disease; silles de la Tourette's syndrome; ss.
                                                               IGS5; infection; pain; cancer; diabetes; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                             anorexia; bulimia; asthma; Parkinson's disease; acute heart
hypotension; hypertension; urinary retention; osteoporosis;
Nucleotide sequence of a human metalloprotease enzyme IGS5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "metalloprotease enzyme IGS5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 5-6; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deleersnijder W, Wiegers R,
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2000EP-0201937.
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                                                               Metalloprotease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypetensive; neuroleptic; neuroprotective; anabolic; anorectic; antiinflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer; haematopoietic; breast; colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAS97159-AAS97195 represent human
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; protease; PCR primer; cytostatic; immunomodulator; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain; immune-related disease; cardiovascular disease; neuronal disease; migraine; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypertension; psychotic disorder; dyskinesia; metabolic disorder; inflammatory disorder; ss.
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                                            Indels
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    Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human metalloprotease partial DNA sequence #15.
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                                                                                                                                                                1257 GATCGGCCACCCTGACTAC 1275
                                                                                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                    1 GATCGCTACCCTGACTAC 19
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89.58;
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    Best Local Similarity 89.5
Matches 17; Conservative
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                         anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; unimary retention; osteoprosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migralne; psychotic disorder; neurological disorder; autism; multiple sclerosis; Azhelmer's disease; neurodegenerative disease; aleep disorder; epilepsy; kidney disease; cardiovascular disease; arterlosclerosis; cerebrovasospasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; ohemotherapy induced injury; tumour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia; Huntington's disease;
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                         subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, motility disorder;
                                                                                                                                                                                                                                                                                           detalloprotease; IGS5; infection; pain; cancer; diabetes; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease, and other neurodegenerative diseases, sleep
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                                                                                                                                                                                                                                                             Nucleotide sequence of a human metalloprotease enzyme IGS5.
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "metalloprotease enzyme IGS5"
 1.2e+02;
                Mismatches
 Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de la Tourette's syndrome; ss.
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1..2262
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                                                                             1413 GATCGGGCACCCTGACTAC 1431
                                                                                                                                                                BP
                                                 GATCGCCTACCCTGACTAC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deleersnijder W, Wiegers R,
                                                                                                                                                             AAF89739 standard; DNA; 2262
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31-MAY-2000; 2000EP-0201937.
31-MAY-2000; 2000NL-1015356.
Best Local Similarity 89.5%;
Matches '17; Conservative
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                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SOLV ) SOLVAY PHARM BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-343815/36.
P-PSDB; AAB83842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200136610-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo saptens
                                                                                                                                                                                                                             23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001
                                                                                                                                                                                             AAF89739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilles
                                                                                                                              RESULT 10
                                                                                                                                               AAF89739
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Human; protease; PRTS-13; enzyme; gastritis; cirrhosis; Crohn's disease; asstrointestinal disorder; autoimmune; inflammatory; cell proliferative; cardiovascular; developmental; epithelial; neurological; reproductive; ordiovascular immune Deficiency Syndrome; allergy; theumatoid arthritis; AIDS; Acquired Immune Deficiency Syndrome; allergy; theumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anaemia, asthma, atherosclerosis, hypertension, myocardial infarction, hepatitis, cancer, psoriasis, Cushing's syndrome, hypothyroidism, eczema, epilepsy, Alzheimer's disease, Huntington's disease, Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pick's disease; infertility; vitiligo; drug screening; gene therapy; ss.
                  cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, Kidney diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, manned disorders, arthritis, endotoxin shock, sepsis, complications of diabetes melilius, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Khan FA;
                                                                                                                                                                                                                                                                                                                                                  Score 15.8; DB 22; Length 2262;
Pred. No. 1.2e+02;
); Mismatches. 2; Indels 0;
cardiovascular diseases, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tribouley CM, Das D, Kallick DA, Nguyen DB, Lee EA, Khi Yue H, Au-Young J, Griffin JA, Policky JL, Ramkumar J, Thangavelu K, Ding L, Kearney L, Baughn MR, Borowsky ML, Sanjanwala MS, Yao MG, Burford N, Walla NK, Lal P, Lee Lo TP, Tang YT, Elliott VS, Azimzai V, T.
                                                                                                                                                                                                                                                                                       Sequence 2262 BP; 520 A; 628 C; 716 G; 398 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mature PRTS-13 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human PRTS-13 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1443 GATCGGGCACCCTGACTAC 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD30580 standard; cDNA; 2318 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                     83.2%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protease, PRTS-13 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-223544P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-224717P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-227568P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-2001; 2001WO-US22397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428..1648
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= · b
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
   epilepsy,
                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200208396-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD30580;
                                                                                                                                                                                                                                                                                                                                                        Query Match
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Todd

Borowsky ML; Lal P, Lee S,

25-MAY-2001.

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PRTS protein and DNA are useful for diagnosing, treating and preventing gastrointestinal disorders (gastritis, cirrhosis, Crohn's disease), autoimmune/inflammatory disorders (AIDS, allergy, rhemmatory arthritis, anaemia, asthma), cardiovascular disorder (AIDS, altergy, rhemmatoria arthritis, anaemia, asthma), cardiovascular disorder (alsorders (hepatitis, cancer, postularis), developmental disorders (Cushing's syndrome, hypothyroidism), epithelial disorders (Cushing's syndrome, hypothyroidism), epithelial disorder (vitiligo, keloid, eczema), neurological disorders (epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease, and reproductive disorders (infertility). PRTS protein is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PRTS DNA is useful for creating knockin humanised animals or transgenic animals to model human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurological disorder, autism; multiple sclerosis; Alzheimer's disease; neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arterlosclerosis; cerebrovasospasm;
                                                                                                                    New human protease polypeptide, useful in diagnosis, prevention and treatment of gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subarachnoid hemorrhage; cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder; gastrioteratinal disorder; gastriote emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion;
                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated human protease polypeptide (PRIS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metalloprotease, IGS5, infection, pain, cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases, in somatic or germline gene therapy and in microarrays utilising fluids or tissues from patients to detect altered PKIN expression. The present sequence is human PRTS-13 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15.8; DB 24; Length 2318;
Pred. No. 1.2e+02;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a human metalloprotease enzyme IGS5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2318 BP; 526 A; 647 C; 735 G; 410 T; 0 other;
                                                                                                                                                                                                                                                                                                                            Claim 5; Page 174-175; 182pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de la Tourette's syndrome; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1502 GATCGGGCACCCTGACTAC 1520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 89.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..2340
WPI; 2002-206082/26.
P-PSDB; AAE19176.
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                                                                                                                                                                                                                                                 disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key.
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The present sequence encodes a human metalloprotease enzyme designated 1GS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, Alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infarction, peripheral vaccular disease, Raynaud's disease, kinney diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ ID NO 18370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2340 BP; 539 A; 649 C; 739 G; 413 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15.8; DB 22;
Pred. No. 1.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                Weske M;
                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 6-7; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1521 GATCGGGCACCCTGACTAC 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL22299/c
ID ABL22299 standard; DNA; 2529 BP.
                                                                                                                                                                                                              Wiegers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                17-NOV-2000; 2000WO-EP11532.
                                                                                                  99NL-1013616.
2000EP-0201937.
                                                                                                                                       31-MAY-2000; 2000NL-1015356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                            (SOLV ) SOLVAY PHARM BV
                                                                                                                                                                                                                                               WPI; 2001-343815/36.
                                                                                                                                                                                                                Deleersnijder W,
                                                                                                                                                                                                                                                                  P-PSDB; AAB83841
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                                                                                                  19-NOV-1999;
31-MAY-2000;
                                                                                   19-NOV-1999;
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10-DEC-2001; 2001WO-IB02399
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                                                        23-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2001
                                                                                                                                                                               Naylor AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF59660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF59660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      á
                                                                                                                                                                                                                         j.
                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                       solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEP; endopeptidase; enzyme; human; neuropeptide Y1; receptor;
male sexual dysfunction; male erectile dysfunction; obesity;
anorexia; bulimia; vasotropic; anorectic; therapy; inhibitor; gene;
                                                                                                                                                                                                                                                             insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                      Score 15.8; DB 23; Length 2529;
Pred. No. 1.3e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not include a stop codon
                                                                                                                                                                              Claim 1; SEQ ID NO 18370; 21pp + Sequence Listing; English.
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8 of the specification'
                                                                                                                                                                                                                                                                                                                                                                        Sequence 2529 BP; 752 A; 721 C; 566 G; 490 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
"5' partial vector sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human SEP endopeptidase coding sequence.
                                                                      Myers EW
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note= "the CDS does
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"the 3' end o
from Figure 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1663 GATCGCTATCCTAACTAC 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABN84280 standard; cDNA; 2580 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= b
product= "SEP"
                                                                     PWD,
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                     Σ
                                                                                                                                                                                                                                                                                                        (ABB57737-ABB72072).
                                                                                             WPI; 2001-656860/75.
                                         (PEKE ) PE CORP NY
                                                                     Adams
                                                                                                                                                    interactions -
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                                                                                                                         New isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                     Venter
                                                                                                                                        genes
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The present sequence is a nucleotide sequence coding for human SEP, a soluble secreted endopeptidase, with an additional 5' coveror partial sequence. The invention relates to the use of an inhibitor of NPY or an inhibitor of NPY I receptor, especially an inhibitor selective for an NPY or NPY II receptor, especially an inhibitor selective for an NPY or NPY II receptor associated with male genitalia, in the preparation of a medicament for the treatment or prevention of male sexual dysfunction, especially male erectile dysfunction (MED). The NPY inhibitor may be used with an auxiliary active agent such as an SEP inhibitor. The invention convides a SEP assay that can be used to detect candidate inhibitors of SEP. In addition to treatment of MED, NPY inhibitors can also be used to treat abnormal drink and food intake disorders, such as obesity, bulimia, anorexia and metabolic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of an inhibitor of neuropeptide Y in the preparation of medicament for the treatment or prevention of male erectile dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 splice variant; alternative splicing; zinc endopeptidase family; neuropeptide; peptide hormone; processing; metabolism; vaccine; drug screening; renal insufficiency; hepatic disease; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.8; DB 24; Length 2580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human neprilysin-like membrane metallopeptidase SNEPb cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2580 BP; 587 A; 741 C; 794 G; 458 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.3e+02;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 8; 179pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1770 GATCGGCCACCTGACTAC 1788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiovascular; hepatotropic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                      Van Der Graaf PH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.58;
                                 2001GB-0009910
2001GB-0008730
                                                                                                                                         2001US-0905846
                                                                                                                                                                              24-AUG-2001; 2001GB-0020679
                                                                      2001GB-0011037
                                                                                                        2001US-0895367
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Matches 17; Conservative
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                                                                                                                                                                                                                                                                                   PFIZ ) PFIZER INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABB79521.
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                                                                  04-MAY-2001;
29-JUN-2001;
13-JUL-2001;
   06-APR-2001;
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99EP-0401767
15-JUL-1999;
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99EP-0401767 15-JUL-1999;

(SNFI) SANOFI-SYNTHELABO

Culouscou J; Jagerschmidt A, Agnel M,

WPI; 2001-212582/22. P-PSDB; AAB60562.

New membrane-associated metallopeptidase SNEPa, SNEPb and SNEPc polypeptides and polynucleotides, useful for treating e.g. acute and chronic renal insufficiency, pain, stroke, cancer, inflammation, renal and hepatic ischemia

Claim 5; Page 30-33; 72pp; English

The invention relates to the human SNEPa, SNEPb and SNEPc proteins, and the cDNAs encoding them. SNEPa, SNEPb and SNEPc are neprilysin-like membrane metallopeptidases and are the products of alternative splicing. The substrate(s) for the SNEP proteins are not as yet known, although the substrate(s) for the SNEP proteins are not as yet known, although the neprilysin family of zinc endopeptidases play key roles in the processing and/or metabolism or neuropeptides and peptide hormones. SNEP conclotides may be used as hybridisation probes for CDNA and genomic DNA; to isolate full-length CDNAs and genomic clones of SNEP homologues; SNEPb or SNEPc; to isolate cDNA and genomic clones of SNEP homologues; as research reagents and material for the discovery of treatments and identification. The SNEP proteins may be used as immunogens to produce antibodies immunospecific for SNEPs, SNEPs or SNEP. SNEP proteins may also be used in screening for compounds which modulate protein, or to purify the proteins by affinity chromatography. SNEP proteins may also be used in screening for compounds which modulate and product mixtures. The SNEP proteins (as vaccine compositions), and product mixtures. The SNEP proteins (as vaccine compositions), and product mixtures in cells, cell-free preparations, chemical libraries and product mixtures and sNEP proteins (as vaccine compositions), content and chronic renal insufficiency, renal and hepatic is chaemia, pain, stroke, hypertensive disease, cancer, inflammation, as restirators or hypertensive disease, cancer, inflammation, restirators or hypertensive disease, cancer, inflammation, as restirators or hypertensive disease, cancer, inflammation, restirators or hypertensive disease, cancer, inflammation, as restirators or hypertensive disease, cancer, inflammation, restirators or hypertensive disease, cancer, inflammation, and set in the proteins and perpeting the proteins and hepetic diseases. well as cardiovascular, neuronal, pancreatic, prostatic, renal, respiratory or hepatic diseases they may also be used in modulating peptide activation and/or degradation in the brain or kidney or in another organ, or to diagnose or treat any disorder related to abnormal expression of SNEPa, SNEPb or SNEPc. The present sequence represents CDNA encoding SNEPb.

Sequence 2636 BP; 601 A; 759 C; 813 G; 462 T; 1 other;

0; Gaps Score 15.8; DB 22; Length 2636; Pred. No. 1.3e+02; 0; Mismatches 2; Indels 0; Indels Ouery Match 83.2%; Best Local Similarity 89.5%; Matches 17; Conservative

1 GATCGGCTACCCTGACTAC 19

δλ qq

1450 GATCGGGCACCCTGACTAC 1468

Search completed: July 8, 2003, 02:19:13 Job time : 120.376 secs

Appli Appli

Sequence 1, A Sequence 1, A Sequence 1, A Sequence 11, Sequence 12, Sequence 16, Se

US-08-906-769-16 US-08-906-616-16 US-08-817-795-16 US-08-485-443B-16

ALIGNMENTS

3-08-485-455D-16 3-08-482-130C-16 3-08-484-211C-16

Sequence Sequence Sequence

US-09-036-987A-1 US-09-370-700-1 US-08-061-465-2 US-08-061-465-1 US-08-361-441B-43 US-09-280-115-121 US-09-792-013-5

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RESULT 1
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Sequence 6, Appli
Sequence 3, Appli
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Sequence 4, p
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                                                                                                                            441362 seqs; 153338381 residues
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Match Length DB
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75.8 4411529
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                             GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: TRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
TITLE OF INVENTION: UNBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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Best Local Similarity 93.8%; Pred. No. 66;
Matches 15; Conservative 0; Mismatches
                                                                                                                                                                                                                        FILE REFERENCE: 2436-0000.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO. 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Mycobacterium tuberculosis
Sequence 2, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-103-840A-1/C
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; Patent No. 180843110N
; APPLICANT: FLEISCHMAN, ROBERT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478219 CGCTACCCCGACTAC 478204
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Appli

08-683-426-1

08-683-426-7 08-683-458-1 08-683-458-7 GENERAL INFORM GENERAL INFORM

08-478-140B-1

Sequence 1, Sequence 3,

Sequence 7, 2 Sequence 1, 2 Sequence 1, 2 Sequence 7, 3 Sequence 7, 3

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Gaps

.: 0

Indels

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: including application
: described below:
08/157,811
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5753488ember 23, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/465,388 FILING DATE: June 5, 1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLILING DATE: NO. 1700., APPLICATION NUMBER: 07/00., TING DATE: May 22, 1992
                                                                                                                                                                              Sequence 6, Application US/08465388 Patent No. 5753488
                                       1 GATCGGCTACCCTGACTAC 19
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                                                                             7 GATCGGATACCCCGTCTAC 25
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TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 567 base pairs
TYPE: nucletc acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 2. FELECOMMUNICATION INFORMATION TELEPHONE: (213) 489-1600 TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
  Conservative
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           Los Angeles
California
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90071-2066
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US-08-465-388-6
                                                                                                                                                                                                                                                                                                                                                                                                         CITY: LOS
STATE: CE
COUNTRY:
    16;
                                                                                                                                                               -08-465-388-6
    Matches
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below:
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT; WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                   Query Match 75.8%; Score 14.4; D
Best Local Similarity 93.8%; Pred. No. 66;
Matches 15: Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5703221ember 23, 1993
APPLICATION NUMBER: 07/887,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,115
FILING DATE: June 5, 1995
CLASSIFICATION: 435
                                                      ; TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
; THER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/301
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                  Sequence 6, Application US/08463115
Patent No. 5703221
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84.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IONE: (213) 489-160
X: (213) 955-0440
67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard
REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 567 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFORMATION FOR SEO ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE CHARACTERISTICS
SOFTWARE: Patentin Ver. SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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90071-2066
                                     4411529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-463-115-6
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Gaps
Length 567;
    DB 1;
              .2e+02;
  Score 14.2; D)
Pred. No. 1.2e.
0; Mismatches
                                                                                                                                          US-09-305-640-3 ; Sequence 3, Application US/09305640B
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Gaps

Length 666; Indels

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74.7%; Score 14.2; DB 1;
84.2%; Pred. No. 1.2e+02;
tive 0; Mismatches 3;
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
APPLICATION NUMBER: 07/887,811
APPLICATION NUMBER: 07/887,502
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
TILLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATORNEY/AGENT INFORMATION:
NAME: WArburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08463115
Patent No. 5703221
                                                                                                                                                                                                                                                    1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                         8 GATCGGATACCCCGTCTAC 26
               ( ) TOPOLOGY: linear US-08-463-115-4
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TELEFAX: (213) 955-0440
TELEX: 67-9510
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.78;
84.28;
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nucleic acid
EDNESS: single
                                                                                                                                                        Query Match
Best Local Similarity 84.2
Matches 16; Conservative
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 666 base pairs
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                  Score 14.2; DB 4; Length 606;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                            NAME/KEX: UNSURE
; LOCATION: (404)(437)(460)(490)(520)(555)(561)(595)
US-09-305-640-3
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PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PREDELICATION NUMBER: 08/157,811
FILING DATE: NO. 5703221ember 23, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
               GENERAL INFORMATION:
APPLICAMY: SMITHKLING Beecham plc
TITLE OF INVENTION: No. 6255468el Compounds
FILE REFERENCE: GP30124
                                                                                          CURRENT APPLICATION NUMBER: US/09/305,640B
CURRENT FILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
LENGTH: 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
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FILING DATE: June 5, 1995
CLASSIFICATION: 435
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May 23, 1992
May 23, 1991
May 23, 1991
NUMBER: 07/763,039
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633 West Fifth Street
Suite 4700
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Patent No. 5703221
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84.28;
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(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 84.28
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                   FEATURE
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Matches

RESULT 8

OD

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; Score 14.2; DB 1;
; Pred. No. 1.2e+02;
0; Mismatches 3;
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                                                                                                                       ISOLATED STEALTH VIRUSES AND RELATED VACCINES
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PRIOR DATE:
PRILING DATE:

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APPLICANT: SmithKline Beecham plc
ATILLE OF INVENTION: NO. 6255468el Compounds
FILE REFERENCE: 6P30124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/305,640B
CURRENT FILING DAFE: 1999-05-05
NUMBER OF SEQ ID.NOS: 4
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/465,388 FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09305640B Patent No. 6255468
                                                                                                                                                                                                                                                                                               E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
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                                            GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: (213) 489-1600 TELEFAX: (213) 955-0440 FELEX: 67-3510 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTORNEY/AGENT INFORMATION:
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Best Local Similarity 84.29
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warburg, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 666 base pairs
nucleic acid
                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          Los Angeles
California
                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90071-2066
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                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: LO:
STATE: C:
COUNTRY:
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STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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    Gaps
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Pred. No. 1.2e+02;
0; Mismatches 3; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            including application described below:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
OF INVENTION:
TOTAL
TOTA
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FILING DATE: No. 5753488ember 23, 1993
APPLICATION NUMBER: 07/887,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATTORNEY,AGENT INFORMATION:
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPALIBLE
COMPUTER: IBM COMPALIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: June 5, 1995
CLASSISTCATION: 435
PRIOR APPLICATION DATA: including appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                660 GATCGGATACCCCGTCTAC 642
                                                                                                                                                                                                                                                                                                                                       US-08-465-388-4
; Sequence 4, Application US/08465388
; Patent No. 5753488
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US-08-465-388-4/c
; Sequence 4, Application US/08465388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GATCGGCTACCCTGACTAC 19
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REGISTRATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 21
FELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.78;
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TELEFAX: (213) 955-0440
TELEX: 67-3310
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 666 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 84.2
Matches 16; Conservative
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 90071-2066
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-465-388-4
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Gaps

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Length 666, Indels

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ic, Nanette H.
Tissue Specific Hypoxia Regulated
Therapeutic Constructs
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APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 14.2; DB 2; Pred. No. 1.5e+02; 0; Mismatches 3;
                                                                                   NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08880342
Patent No. 6218179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Webster, Keith A.
Bishopric, Nanette H.
Murphy, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE TOCKET NUMBER: 925
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5057 base pairs
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                 Bishopric,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                             APPLICANT: Bishopri
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                               Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Webste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                         94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-365-486A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-880-342-12
           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                       Length 2560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14.2; DB 1; Length 4224;
Pred. No. 1.4e+02;
0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Peery, Robert B
APPLICANT: Skatrud, Paul L
APPLICANT: Thornewell, Susan J
TITLE OF INVENTION: MULTIFLE DRUG RESISTANCE GENE OF
TITLE OF INVENTION: CRYPTOCOCCUS NEOFORMANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,521
                                                                                                     Score 14.2; DB 4;
Pred. No. 1.4e+02;
                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08365486A
Patent No. 5834306
                                                                                                                                                                                                   1752 GGTCGCTACCCGGACTTC 1770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Patent Division/AEH
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4147 GCTCGGCTACCCTGCCTTC 4129
                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08612521
Patent No. 5786463
                                                                                                                                                                               1 GATCGGCTACCCTGACTAC 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: X
TELECOMMUNICATION INFORMATION
TELEPHONE: 317-276-3169
                                                                                               74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hamilton, Amy E
REGISTRATION NUMBER: 33,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317-276-1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Patent D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
LENGTH: 2560
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46285
                                                                                                                                                                                                                                                                             RESULT 11
US-08-612-521-1/c
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US-08-365-486A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-612-521-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                           US-09-305-640-1
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Length 5057; Indels

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0; Gaps
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Patent No. 554553
GENERAL INFORMATION:
APPLICART: GOSCOLLICH, EMIL C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 5108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/312,387B
FILING DATE: Ully 7, 1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742;
REGISTRATION NUMBER: 26,742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 1;
Pred. No. 1.5e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2175 GATCGCCGTCCGTGACTAC 2193
                 CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGEN, SATAh.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 296-780
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 133521
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 5859 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                    5108 base pairs
  19910118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 343-1684
                                                                                                                                                                                                                                                        TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 400..4686
; OTHER INFORMATION:
US-07-642-002-1
                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Rattus ration TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New COUNTRY: US ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JS-08-312-387B-1
                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bredt, David S.
APPLICANT: Hwang, Paul M.
APPLICANT: Reed, Randall
APPLICANT: Snyder, Solomon H.
TITLE OF INVENTION: Purification and Molecular Cloning of Nitric FITLE OF INVENTION: Oxide Synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 14.2; DB 4; Length 5057;
Pred. No. 1.5e+02;
0; Mismatches 3; Indels 0
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 23-JUN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: One Thomas Circle, NW
CITY: Washington
                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IB95/00996
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8255-0018.30
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: rat bNOS CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIE: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCHAPTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2124 GATCGGCGTCCGTGACTAC 2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07642002
Patent No. 5268465
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 74.7%;
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 5057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
349..4638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Linear
MOLECULE TYPE: CDN?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION:
US-08-880-342-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
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STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURE:
ORGANISM: Neisseria gonorrheae.
STRAIN: F62
FEATURE:
NAME/KEY: CDS
LOCATION: 1.381
FEATURE:
NAME/KEY: CDS
LOCATION: 445.1491
FEATURE:
NAME/KEY: CDS
LOCATION: 2342.3262
FEATURE:
NAME/KEY: CDS
LOCATION: 3322.4335
FEATURE:
NAME/KEY: CDS
LOCATION: 3322.4335
LOCATION: 4354.5196
US-08-312-3878-1
```

0; Gaps

Query Match 74.7%; Score 14.2; DB 1; Length 5859; Best Local Similarity 84.2%; Pred. No. 1.5e+02; Matches 16; Conservative 0; Mismatches 3; Indels 0;

Search completed: July 8, 2003, 09:32:41 Job time: 38.2793 secs

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(without alignments)
273.390 Million cell updates/sec
                                                                                                       July 8, 2003, 19:09:54; Search time 109.737 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   1105431 seqs, 789497651 residues
                                                                OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                            US-09-647-780A-19
                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Segmence 4. Appl 4	Sequence 1. Appli	``	'n	~	Sequence 65, Appl	Sequence 294, App	Sequence 92943, A	Sequence 4481. Ap	Sequence 326, App	Sequence 8224, Ap	Sequence 326, App	Sequence 97871, A	Sequence 4455, Ap	Sequence 156, App		Sequence 51979, A	Sequence 510, App	Sequence 510, App
		į														•				
	ID QI	US-10-017:273A-4	US-09-905-846-1	US-10-017-273A-5	US-09-905-846-5	US-09-938-842A-2328	US-09-910-664-65	US-09-770-445-294	US-10-098-263B-92943	US-09-294-093B-4481	US-10-091-483-326	US-09-764-891-8224	US-09-764-846-326	US-10-098-263B-97871	US-10-156-761-4455	US-10-037-270-156	US-10-156-761-1	US-10-098-263B-51979	US-10-046-935-510	US-08-878-178-510
•	89	. 6	10	6	10	σ	σ	10	σ	10	6	6	10	σ	σ	σ	σ	6	ڻ	6
	Length DB	2893	2893	2975	2975	432	574	296	25	306	5250	5250	5250	25	840	4053	9025608	25	200	200
æ	Query Match	83.2	83.2	83.2	83.2	81.1	81.1	81.1	77.9	77.9	77.9	77.9	77.9	75.8	75.8	75.8	75.8	74.7	74.7	74.7
	Score	15.8	15.8	15.8	15.8	15.4	15.4	15.4	14.8	14.8	14.8	14.8	14.8	14.4	14.4	14.4	14.4	14.2	14.2	14.2
	Result No.		8	m	4	υ Ω	9	٥ /	ω υ	ი ა	10	c 11	12	c 13	c 14	c 15	c 16	c 17	c 18	c 19

Sequence 510, App	Sequence 550, App	Sequence 1019, Ap	Sequence 1019, Ap	Sequence 1019, Ap	Sequence 1019, Ap		m	ריי	Sequence 37957, A	Sequence 9905, Ap	Sequence 3, Appli	67,	Sequence 99, Appl	101,	Sequence 107, App	Sequence 109, App	Sequence 523, App	Sequence 1151, Ap	Sequence 124, App	Sequence 122, App	-	Sequence 13, Appl	7	116	Sequence 119, App
9 US-10-146-502-510	10 US-09-960-352-550	9 US-09-736-457-1019	9 US-09-902-941-1019	9 US-09-849-626-1019	9 US-10-017-754-1019	9 US-09-918-995-17948	9 US-10-156-761-3748	9 US-09-918-995-37923	9 US-09-918-995-37957	9 US-10-198-846-9905	9 US-09-798-723-3	9 US-09-453-234-67	9 US-09-453-234-99	3 US-09-453-234-101	3 US-09-453-234-107	9 US-09-453-234-109	10 US-09-974-300-523	10 US-09-954-456-1151	9 US-10-171-311-124	9 US-10-171-311-122	10 US-09-974-300-6007	3 · US-10-166-087-13	US-09-798-723-1	US-10-028-072-119	US-10-121-049-119
200	. 300	348	348	348	348	355	456	495	496	.562	909	675	675	675 9	675	675	990	1008	1066	.1081	1107	1866 9	2560 9	2868 9	2868
74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7	74.7
14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	. 14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2	14.2
c 20	21	c 55	c 23	c 24	c 25	26	27	c 28	c 29	30	31	32	33	34	35	36	37	38	39	40	. c 41	42	43	44	. 45
								,													•				

ALIGNMENTS

Published Applications NA:

Database :

	Dysfunction			Length 2893; Indels 0;
A-4 Applicati No. US200 ORMATION: Pfizer In Naylor,	CANT: Van Der Graaf, Pieter H GANT: Waynan, Christopher P. OF INVENTION: Treatment of Male Sexual REFERENCE: PC22013 NT APPLICATION NUMBER: US/10/017,273A NT FILING DATE: 2001-12-12 APPLICATION NUMBER: US 60/265,358	FILING DATE: APPLICATION FILING DATE: PEDING DATE: APPLICATION FILING DATE: APPLICATION FILING DATE:	PRIOR FILING DATE: 2001-07-13 PRIOR FILING DATE: 2001-07-13 PRIOR PLICATION NUMBER: US 60/291,722 PRIOR PLICATION NUMBER: US 60/291,722 PRIOR PLICATION NUMBER: US 09/895,367 PRIOR PELICATION NUMBER: US 09/895,367 PRIOR FILING DATE: 2001-06-29 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin version 3.1 SEQ ID NO 4	: LENGTH: 2893 : TYPE: DNA : ORGANISM: Homo sapiens US-10-017-273A-4 Query Match BS: Local Similarity 89.5%; Fred. No. 41; Matches 17; Conservative 0; Mismatches 2;

Gaps

1705 GATCGGGCACCTGACTAC 1723

Db

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PPLICANT: Wang, Xun
PPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAIN:
TITLE OF INVENTION: SAME, AND METHODS OF USE
ILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                              APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE REFERENCE: PCS10926Apms: US/09/905,846
CURRENT APPLICATION NUMBER: US/09/905,846
CURRENT FILING DATE: 2001-07-13
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 60/220,908
PRIOR FILING DATE: 60/220,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15.8; Di
Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 15.4;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NOWER: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/300,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2328, Application US/09938842A
Patent No. US20020160378A1
                                        1770 GATCGGGCACCCTGACTAC 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1770 GATCGGCCACCTGACTAC 1788
                                                                                                                                                      Sequence 5, Application US/09905846 Patent No. US20020102707A1
1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATCGGCTACCCTGACTAC 19
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nilarity 94.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.2%;
ilarity 89.5%;
Conservative
                                                                                                                                                                                                                           APPLICANT: Ian Dennis Harrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2328
LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                   US-09-905-846-5
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    õ
                                                                                                                              APPLICANT: Ian Dennis Harrow
APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE REFERENCE: PCS10926APME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPPLICANT: Naylor, Alasdair M.
PPLICANT: Van Der Graaf, Pieter H
PPLICANT: Wayman, Christopher P.
IIILE OF INVENTION: Treatment of Male Sexual Dysfunction
ILE REFERENCE: PC22013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
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Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
83.2%; Score 15.8; D
Best Local Similarity 89.5%; Pred. No. 41;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/905,846
CURRENT FILING DATE: 2001-07-13
PRIOR PRIOR PILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 8
SCOTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/017,273A CURRENT FILING DATE: 2001-12-12
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PRIOR PELICATION NUMBER: GB 0108930.3
PRIOR PELICATION NUMBER: GB 0120679.6
PRIOR PELICATION NUMBER: GB 0120679.6
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/291,722
PRIOR APPLICATION NUMBER: US 60/291,722
PRIOR PELICATION NUMBER: US 09/895,367
PRIOR FILING DATE: 2001-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URRENT FILING DATE: 2001-12-12
RIOR APPLICATION NUMBER: 05 60/265,358
RIOR FILING DATE: 2001-01-31
RIOR APPLICATION NUMBER: GB 0030647.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1705 GATCGGGCACCCTGACTAC 1723
                                                                Sequence 1, Application US/09905846
Patent No. US20020102707A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATCGGCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-905-846-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-017-273A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pfizer Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBE: Paten-
SOFTWARE: Paten-
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Gaps

Indels

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Happlicant: Lalgudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR PRICATION NUMBER: 60/082,567
PRIOR PELING DATE: April 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700354371H1
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 92943
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 14.8; DB 9;
Pred. No. 1.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: 2, 66, 70, 74, 85, 91, 201, 290, 298
; OTHER INFORMATION: a, t, c, q, or other
US-09-294-093B-4481
                                                                                                                                                                                       Sequence 93943, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TILE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
Best Local Similarity 94.1%; Pred. No. 70; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATCGGCTACCCTGACTA 18
                                                                             182 TCGGCTGCCTGACTAC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ATCGGCTACCCTGACTAC 19
                                                       3 TCGCCTACCCTGACTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.9%;
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88.9%;
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Best Local Similarity 88.9°
Matches 16; Conservative
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Matches 16; Conservative
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US-10-098-263B-92943
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US-09-294-093B-4481/c
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LENGTH: 306
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                                                                                                                                                                                                            TITLE OF INVENTION: METHODS OF CREATING DWARF PHENOTYPES IN TITLE OF INVENTION: PLANTS
FILE REFERENCE: 008010189000018
CURRENT APPLICATION NUMBER: US/09/910,664
CURRENT FILLING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 574
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Pred. No. 73
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09770445
                                                                         Sequence 65, Application US/09910664
Publication No. US20020194646A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: POGUE, Greg P.
PSPLICANT: DELLA-CIOPPA, GUY R.
APPLICANT: WOLFE, Gerson M.
APPLICANT: ZHENG, Wenjin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TCGGCTACCCTGACTAC 19
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US-09-910-664-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Arabidopsis thaliana
US-09-770-445-294
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Price, Jennifer L.
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94.1%;
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis, Keith R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE:
                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 294
LENGTH: 967
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Gaps

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Indels

Length 25;

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 Length 306;
Score 14.8; DB 10;
Pred. No. 1.6e+02;
0; Mismatches 2;
                                                                         59 GATCGGCTCCCCTGACCA 42
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Score 15.4; DB 10; Length 967;

81.18;

Query Match

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Gaps
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                                                                                           Length 5250;
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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                                                                                        Score 14.8; DB 10;
Pred. No. 1.3e+02;
0; Mismatches 2;
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Pred. No. 2.4e+02;
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Pred. No. 2.9e+02;
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TITLE OF INVERFION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
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CURRENT FILING DATE: 2002-05-29
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PRIOR FILING DATE: 2001-05-30
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PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 97871, Application US/10098263B Publication No. US20030104410A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4455, Application US/10156761
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                                                                                                                                                                                                                                                                 2981 GATCTGCTTCCCTGACTA 2998
                                                                                                                                                                                                                            1 GATCGGCTACCCTGACTA 18
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                                                                                           77.98;
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HORIKAWA, HIROSHI
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                                                                Query Match
Best Local Similarity 88.5.
Best Local 16; Conservative
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Best Local Similarity 93.84
The state of the 
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NUMBER OF SEQ ID NOS: 15109
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; ORGANISM: Homo sapiens US-09-764-846-326
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US-10-098-263B-97871
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Best Local Similarity
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 326
LENGTH: 5250
TYPE: DNA
                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PIZICAL
CURRENT APPLICATION NUMBER: US/10/091,483
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 348
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Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
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Pred. No. 1.3e+02;
); Mismatches 2;
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1.3e+02;
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Pred. No. 1.3e-
0; Mismatches
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Publication No. US20030077808A1
                                                                                        Sequence 326, Application US/10091483 Publication No. US20030049650A1
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 88.9%;
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-10-091-483-326
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; ORGANISM: Homo sapiens
US-09-764-891-8224
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US-09-764-891-8224/c
                       RESULT 10
US-10-091-483-326
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0; Gaps
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TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
 1; Indels
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                      Sequence 156, Application US/10037270 Publication No. US20030104529A1 GENERAL INFORMATION:
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LOCATION: (409)..(3819)

NAME/KEY: misc_feature

LOCATION: (1)...(4053)

OTHER INFORMATION: n = a,t,c or g

US-10-037-270-156
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SOFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 156
LENGTH: 4053
                                                         541 GATCGCCGACCTGAC 526
                                   1 GATCGGCTACCCTGAC 16
 15; Conservative

    Yonghong
    Jian-Rui
    Ping

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Liu, Chenghua
Asundi, Vinod
Zhang, Jie
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Wang, Dunrui
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Matches
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Query Match 75.8%; Score 14.4; DB 9; Length 4053; Best Local Similarity 93.8%; Pred. No. 2.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; G

Search completed: July 9, 2003, 02:22:37 Job time: 113.787 secs

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16: em estom:*	BF798255		
	LOCUS	BF798255	268 bp
18: em_gss_hum:*	DEFINITION	RC4-CI0118-021000-011-502	10118
20: em_gss_rin;	VERSION	BF798255.1 GI:12127244	
	KEYWORDS		
22: em_gss_run:* 21: em_gss_run:*	SOURCE	TSW Homo sapiens	
		Eukaryota; Metazoa;	
		Mammalia;	s; Cai
27: em_gss_pro:*	REFERENCE	CE I (Dases 1 to 208) RS Dias Neto,E. Garcia Correa,R	2
		Nagal, M.A., da Silva,	
No. is the number of results predicted by chance to have		Goldman, G.H., Carvalho, A.F.,) Mats
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		lvella, r. Brentani,	
		Simpson, A.J.	
SUMMARIES	TILLE	Shotgun sequencing of the human	uwan
	JOURNAL	Proc. Natl.	A. 97
No. Score Match Length DB ID Description	MEDLINE	NE 20202663	

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ALOGRSOS AUDGBSOS AZB60366 2M0166N18 AUGBSCOB AUGBSCOB AA965735 049041.r ALB37034 ALB37034 ALB37034 ALB37034 A1978418 R2530.R E BPC009157 SS74f08.y BBZ79096 BBZ78096 BBZ88846 601513766 AN155204 mg1e0002D AN155204 mg1e0002D R84027 15986 Lambd 229058 ATTS2071 Or BQ459214 HA01P011r BB444927 BB444927 R30332 12937 Lambd	AA712729 32288 Lam AV562561 AV562561 T21346 3954 Lambda T22584 4592 Lambda AV526345 AV226345 BB870158 BB870158 BF046319 BF2500028 R90649 17004 Lambda T44898 5161 Lambda T21763 3771 Lambda AA042552 25064 Lam T44972 8235 Lambda AV818992 AV818992	AV531738 AV531738 R64763 13267 Lambd AV530491 AV530491 T75790 10568 Lambd BF419565 UI P-CAO- M40463309 BP230012A BE470647 WHE0262_E H7717 17608 Lambd R8437 12133 Lambd R84020 15979 Lambd	r .EST 12-JAN-2001 NA, mRNA sequence. ta; Euteleostomi; dae; Homo. a,S., Briones,M.R., Costa,F.F., G.S., Simpson,D.H., eel,(V.V., O'Hare euter, V.Y., O'Hare	ORF exp
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 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 000 6 0 000 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 BF798255 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL MEDLINE COMMENT

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                              /note-"Organ: colon_ins; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC4&t2=RC4_CI0118-021000-011-b02&t3=2000-10-02&t4=1)
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1 (bases 1 to 564)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsla, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
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crown cDNA library Triticum
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16.4; DB 12; Length 268;
Pred. No. 8.2e+02;
); Mismatches 1; Indels 0
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Tel: 5105595773
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/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                'organism="Homo sapiens'
'db_xref="taxon:9606"
                                                                                                                 Seq primer: puc 18 forward
High quality sequence start: 81
High quality sequence stop: 268
Location/Qualifiers
asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                          /clone_lib="CI0118"
/dev_stage="Adult".
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/organism-"Homo
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94.4%;
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pullescript SK Site. 1 EcoR1, Site. 2: Mnoi; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, mystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Research Service, Pacific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 25-JUL-2000
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                   Site_1: ECORI; Site_2: Mol; Seeds were germinated and grown at 4 C for 5 weeks. The tissue, total RNA, and poly(A) RNA were prepared, a CDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="Wheat etiolated seedling root normalized cDNA
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WHE1129_C05_E092S Wheat etiolated seedling root normalized CDNA
library Triticum aestivum CDNA clone WHE1129_C05_E09, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq.primer: Stratagene SK primer.
note="Vector: Lambda Uni-ZAP XR, excised phagemid;
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                                                                                                                         phagemids in the TJ Close lab (Choi, Close, Fer
the University of California, Riverside. Plass
preparations and DNA sequencing were performed
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                Length 564;
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West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                   Score 16.4; DB 10;
Pred. No. 1.1e+03;
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/db_xref="taxon:4565"
/clone-"WHE1129_C05_E09"
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BE444890.1 GI:9444442
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Best Local Similarity 94.4%;
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261 bp mRNA linear EST 03-MAY Gm-c1052 Glycine max cDNA clone SOYBEAN CLONE ID: 0 5' similar to TR:Q9SX30 Q9SX30 F24J5.9.; mRNA

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I, Fabales, Fabaceae, Papillonoideae, Phaseoleae,
                                                                                                                                                                                                                     BQ252570.1 GI:2044846
  91 ATCGGCTACACTGACTAC 74
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Gm-c1052-5650
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                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                  RESULT 5
BQ252570
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                                                                                                              LOCUS
  Dp.
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//dev_stage="Feekes' scale 1"
//note="vector: Lambda Unl-ZAP XR, excised phagemid;
Site_1: EcoRi; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov-
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polya was purified from the pooled from the two
samples, polya was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov-Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST .09-APR-2002
                           Nguyen
                      phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Y. Ogihara unpublished cDNA library, Wh_r"/tissue_type="root"
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               BJ283075 Golhara unpublished cDNA library, Wh.r Triticum aestivum cDNA clone whrl4d05 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.4; DB 13; Length 667;
Pred. No. 1.2e+03;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                              Score 16.4; DB 10; Length 580; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              performed in the OD Anderson lab (all other 192 c 179 g 149 t
    The mass
                                                                                                                                                                                                                                              Indels
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                    preparations and DNA sequencing we
Anderson lab (all other authors)."
155 c 162 g 134 t
normalization was carried out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preparations and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expressed genes in Triticum aestivum Unpublished (2002)
                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="whr14d05"
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                                                                                                                                                                                                                                                                                          2 ATCGGCTACCCTGACTAC 19
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Ogihara,Y. and Murai,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Tadasu Shin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.3%;
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llarity 94.4%;
Conservative
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                                                                                                                                                                                                            Local S. 17;
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Matches
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JOURNAL
COMMENT
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SOURCE
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhOI; The Harosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The CDNA library was constructed from mRNA isolated from whole seedlings of I week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3 anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhOI digestion. The CDNA fragments were directionally cloned into the EcoRI-XhOI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact: ccu@resgen.com web site:
Shoemaker, R., Kein, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra; M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, P.R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GibcoBRL). The library was constructed in cooperation
                                                                                                                                                                                                                                                                       Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paul Keim's Laboratory at Northern Arizona
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                                                                                                                                                                                                                                                                 Contact: Shoemaker R/Public Soybean EST Project
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Pred. No. 1.6e+03;
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/clone_lib="Gm-c1052"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: -40RP from Gibco
High quality sequence stop: 183.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.2%;
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                                                                                                                                                                                                                                      Unpublished (1999)
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Best Local Similarity
Matches 17; Conserv
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Gaps

94.48;

Best Local Similarity

17; Conservative

Matches

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AZ860366.1 GI:13055614
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1 (bases 1 to 360)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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                                   PROJECT = 'RGP'
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ORIGIN
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AZ860366
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                                                                                             D22128
RICC10388A Rice callus Oryza sativa (japonica cultivar-group) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 01-APR-2002
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pBluescript II SK+; Site_1: SalI; Site_2: NotI; Onba prepared from rice callus mRNAs by using oligo(dT) as a primer and ligating to the SalI-NotI site of pBluescript II SK+ phagemid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU068505 ALCE Callus Oryza sativa (japonica cultivar-group) CDNA
                                                                                                                                                                                                                                                                                                                                                                           National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group)
Sukaryota, Virdólplantee, Streptophyta; Embryophyta; Trach
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.2%; Score 15.8; DB 14; Length 304; 89.5%; Pred. No. 1.7e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone C30382_4A, mRNA sequence.
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                                                                                                                                  lone C10388_1A, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice cDNA from callus (1998)
Unpublished (1998)
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namoto, K. and Sasaki, T.
GATGGGCTTCCCTGACTAC 72
                                                                                                                                                                                                                                                                                                   1 (bases 1 to 304)
Sasaki, T. and Minobe, Y.
Rice cDNA from callus
Unpublished (1994)
Contact: Takuji Sasaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                     3602, Japan
81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 81-298-38-7468
                                                                                                                                                                      D22128.1 GI:431794
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DEFINITION
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AUTHORS
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AU068505
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                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA
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2M0166N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0166N18 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,
84112, USA
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                                                                                    /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 335;
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musculus C57BL/6J (male) was obtained
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

83.2%; Score 15.8; DB 9;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0166 row: N column: 18
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Location/Qualifiers
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/clone="UUGC2M0166N18"
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Best Local Similarity
Matches 17; Conserv
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AA965735/c
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DEFINITION
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwDA2 (gil4732114|gb)AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ลงบอเอบช
AU082608 Rice callus Oryza sativa (japonica cultivar-group) cDNA
clone C30226, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="coace"
/clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site_I: SalI; Site_2:
NotI: cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tsasak1@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachi
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Pred. No. 1.8e+03;
0; Mismatches 2; Indels 0;
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Pred. No. 1.8e+03;
); Mismatches 2;
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Rice CDNA from callus (2000)
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AU082608.1 GI:7134660
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Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-298-38-7468
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Best Local Similarity 89.5
Matches 17; Conservative
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Local S....
17;
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AU082608
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208 GATCGGCTACCTGGATAC 226

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AL837034 EFRf Takifugu rubripes cDNA clone EFRf027apcP22, mRNA
         EST 31-JUL-1998
AA965735.
04g04al.rl Aspergillus nidulans 24hr asexual developmental and vegetative CDNA lambda zap library Emericella nidulans CDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: broe@ou.edu
We anticipate the future release of the CDNA clones to the Fungal
Genetics Stock Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                      Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
1 (bases 1 to 377)
                                                                                                                                                                                                                                                                     (upfer,D., Gray,J., Hausner,J., La1,H., Martin,W., Aramayo,R.
                                                                                                                                                                                                                                                                                                                                                      Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
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llarity 89.5%; Pred. No. 1.8e+03;
Conservative 0; Mismatches 2;
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High quality sequence stop: 281.
Location/Qualifiers
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                                                                        04g04a1 5', mRNA sequence
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1 (bases 1 to 396)
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                                                                                                               AA965735.1 GI:3139619
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Unpublished (2002)
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                                                                                                                                                                                                                                                                                           Prade, R. and Roe, B.
                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
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Takifugu rubripes
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Fax: 405 325 7762
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated
                                                                                                                                                                                                                                                                                                                             Score 15.8; DB 9; L
Pred. No. 2e+03;
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High quality sequence stop: 417.
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                                                                                                                                   /db_xref="RiceGenes:R2530"
/db_xref="taxon:4530"
/clone="R2530"
                                                                                                  /organism="Oryza sativa"/cultivar="IR36"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Glycine max"
/db_xref="taxon:3847"
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                                         Seq primer: M13 Reverse
                      BACKWARD: M13 Reverse
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Fax: 314 286 1810
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Public So
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ars-genome.cornell.edu/cgi&2Dbin/WebAce/webace?db=ricegenes&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta Spermatophyta; Magnoliophyta; Liliopsida: Poales; Poaceae; Enhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 439)
Causse, M.A., Fulton, T.M., Cho, Y.G., Ahn, S.N., Chunwongse, J., Wu, R. Aioo, J., Yu, Z., Ronald, P.C., Harrington, S.E., Second, G., McCouch, S.R. and Tanksley, S.D. Saturated molecular map of the rice genome based on an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RZ530.R ECORI Rice Eticlated Leaf cDNA Library Oryza sativa cDNA clone RZ530, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Minnesota. For mapping information, additional citations and other related information concerning this probe, please refer to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                               Library created by Greg Elgar
MRC Human Genome Mapping Project Resource Centre, Hinxton,
Cambridge, CB10 1SB. UK
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                    MRC Human Genome Mapping Project Resource Centre
Hinxton, Cambridge, CB10 1SB, UK
Email: biohelp@hgmp.mrc.ac.uk
                                                                                                                                                            The clone can be obtained from www.hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Err."
/tissue_type="brain"
/note="Vector: pBluescript II KS"
94 q 101 t
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Pred. No. 1.9e+03;
0; Mismatches 2;
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Senetics 138 (4), 1251-1274 (1994)
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/clone_lib="EFRf"
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                                                                                  Email: biohelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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el: 607 255 0420
ax: 607 255 6683
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PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RiceGenes database at
                                                                                                  Vector: pBluescript II KS
V_type: phagemid
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Contact: Clark MS
MRC Human Genome
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DEFINITION
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Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF009157 505 bp mRNA linear EST 06-DEC-2001 ss74f08.yl.Gm-c1062 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1062-2176 5' similar to TR:Q9SX30 Q9SX30 F24J5.9 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Shoemaker, Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
/clone_lib-"EcoRI Rice Etiolated Leaf cDNA Library"
/note="Vector: pBLUESCRIPT; Derived from mRNA extracted
from etiolated leaf sheath from the cultivar IR36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="stem tissue of greenhouse grown.plants"
/dev_stage="1 month old"
                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 2334 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'clone-"GENOME SYSTEMS CLONE ID: Gm-c1062-2176"
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                                                                                                                                                                                                                                                                            Length 439;
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Soybean EST Project
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Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001).
                                                                                                                                                                                                                                    of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GlbcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker." a 94 c 126 g 129 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB279096 RIKEN full-length enriched, adult retina Mus musculus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST, 24-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Carnindi,r.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Car Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                       directionally cloned into the EcoRI-XhoI restriction site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Cranjata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 .(bases 1 to 659)
                                                                                                                                  were ligated to the blunt-ended cDNA fragments
month old greenhouse grown plants
                                                                                                     restriction site. EcoRI
                     for the cultivar Raiden. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                   followed by XhoI digestion. The cDNA fragments were
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K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jul 7, 2000 this sequence version replaced gi:8976118 Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8; DB 12
Pred. No. 2.1e+03;
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stem tissue of 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 83.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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BB279096
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BEST 20-OCT-2000 601513766F1 NIH_MGC_71 Homo sapiens CDNA clone IMAGE:3914848 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   whose assistance we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN. Division of Experimental Animal Research in Riken
                                                                                                             Encyclopedia Project of Genome Exploration Research Group in Rike
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      provided by Stefano Gustincich,
logy, Harvard Medical School, 220
Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                   'clone_lib="RIKEN full-length enriched, adult retina"
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse
                     Human Genome Sequences Mamm: Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
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GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'],
                                                                                                                                                                                                                                                                                                                                                                                                                'note="Site_1: SalI; Site_2: BamHI; cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
;
                                                                                        cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Gro
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
1 (bases 1 to 851)
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Longwood Ave., Boston, MA02115, USA,
gratefully acknowledge."
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Pred. No. 2.
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                                                                                                                                                                                                                                                     organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                tissue_type="retina"
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/lab_host="DH10B"
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
plate: LLAM9737 row: d column: 17
High quality sequence stop: 683.
Location/Qualifiers
I. 851
Corganism="Homo sapiens"
/Ab_aref="Haxon:9606"
/Clone="InAGE:3914448"
/Clone="InAGE:391448"
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//Lab_host="PhiloB" (phage-resistant)"
//Lab_host="DhiloB" (phage-resistant) (note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
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Job time: 967.404 secs
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	July 8, 2003, 00:45:53; Search time 209.093 Seconds (without alignments) 2644.537 Million cell updates/sec
Title:	US-09-647-780A-20
Sequence:	1 gttcgccatccagtccatc 19
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2054640 segs, 14551402878 residues
Total number of	Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0	Minimum DB seq length: 0 Maximim DB sec length: 200000000

Post-processing: Minimum Match 008
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36: em_htg_mam:*
37: em_htg_wrt:*
38: em_htg_other:*
40: em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	19 bp	WO9953077						-		Ouimet, T.		talloprote	rapy
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	AX014720	Sequence 20 from Patent WO9953077.	AX014720 7	AX014720.1 GI:10040993		synthetic construct.	synthetic construct	artificial sequences.	1 (bases 1 to 19)	Schwartz, J.C., Gros, C., Ouimet, T., Rose, C., Bonhomme, M.C. and	Facchinetti, P.	Novel nep ii membrane metalloprotease and its use for screening	inhibitors useful in therapy
AX014720	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS		TITLE	

PAT 08-JUN-2001

JOURNAL

FEATURES

BASE COUNT ORIGIN

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Plowman, G.D., Whyte, D., Sudarsanam, S., Manning, G., Caenepeel, S. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Deleersnijder,W., Wiegers,R. and Weske,M.
Human enzymes of the metalloprotease family
Patent: WO 0136610-A 1 25-WAY-2001;
Solvay Pharmaceuticals B.V. (NL)
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Patent: WO 0183782-A 28 08-NOV-2001;
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Sequence 28 from Patent WO0183782.
AX319864
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nep 11 membrane metalloprotease and its use for screening
                   TE JEAN CHARLES (FR); GROS CHRISTIANE (FR); BONHOMME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN CHARLES (FR); GROS CLAUDE (FR); OUIMET TANJA (FR); ROSE CHRISTIANE (FR); BONHOMME MARIE CHANTAL (FR); FACCHINETTI PATRICIA (FR)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 2765).
Schwartz,J.C., Gros,C., Ouimet,T., Rose,C., Bonhomme,M.C. and
Facchinetti,P.
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               INST NAT SANTE RECH MED (FR); SCHWARTZ JEAN C. CLAUDE (FR); OUINET TANNA (FR); ROSE CHRISTIA MARIE CHANTAL (FR); FACCHINETIT PATRICIA (FR) LOCATION/QUALLIFIES
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                                                                                                           /organism="synthetic construct"
/db_xref="taxon:32630"
/note="oligonucleotide"
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Pred. No. 84;
                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitors useful in therapy
Patent: WO 9953077-A 1 21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus rattus"
/db_xref="taxon:10117"
                                                                                                                                                                                                                         Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AX014701 2765 bp Sequence 1 from Patent W09953077.
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                                                                                                                                                                                                                       th 100.0%;
| Similarity 100.0%;
| 19; Conservative 0
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ilarity 100.0%;
Conservative 0
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Best Local Similarity
...hes 19; Conserva
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Best Local S
Matches 19
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ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

LOCUS

RESULT 2 AX014701

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PAT 14-DEC-2001

BASE COUNT ORIGIN

Vertebrata; Euteleostomi;

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DRPAVEKARTLYRSCMNQSVIEKRGSQPLLDILEVVGGWPVAMDRWNETVGLEWELER
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                             1 (bases 1 to 2340)
Deleersnijder,W., Wiegers,R. and Weske,M.
Human enzymes of the metalloprotease family
Patent: WO 0136610-A 3 25-MAY-2001;
Solvay Pharmaceuticals B.V. (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.4; DB 6;
Pred. No. 5.1e+02;
0; Mismatches 1;
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Pred. No. 5.1e+02;
); Mismatches 1;
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Patent: WO 0226958-A 3 04-APR-2002;
MILLENNIUM PHARMACEUTICALS, INC. (US)
                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 3 from Patent W00226958.
AX473102.1 GI:22207836
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/db_xref="taxon:9606"
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                                                                                                                                              Location/Qualifiers
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ilarity 94.7%;
Conservative
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nilarity 94.7%;
Conservative 0
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Matches 18; Conserv
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Best Local Similarity
Matches 18; Conserv
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AX473102
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                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                     Length 2232;
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Pred. No. 5.1e+02;
0; Mismatches 1; Indels 0
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Human enzymes of the metalloprotease family
Patent: WO 0136610-A 5 25-MAY-2001;
Solvay Pharmaceuticals B.V. (NL)
                                                                           Score 17.4; DB 6;
Pred. No. 5.1e+02;
0; Mismatches 1;
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                                     395
/organism="Homo sapiens"
/db_xref="taxon:9606"
620 c 705 g 395
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Sequence 5 from Patent W00136610.
AX146980.1 GI:14346251
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/db_xref="taxon:9606"
1. .2262
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Sequence 3 from Patent WO0136610.
AX146978
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                                                                                                                                               2082 GTTCGCCATCCAATCCATC 2100
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                                                                           91.68;
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ilarity 94.7%;
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Best Local Similarity
Matches 18; Conserv
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AX146980
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AX146978
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PAT 09-AUG-2002

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

AF302075

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ORGANISM

REFERENCE AUTHORS

TITLE

us-09-647-780a-20.rge

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'note="SEP(delta); metalloprotease; alternatively spliced"
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LADNQNVNGFSSLGENIADNGGVRQAYKAYLRWLADGGKDQRLFGLNLTYAQLFFINY
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                                                                                                                                                  Molecular identification and characterization of novel membrane-bound metalloprotease, the soluble secreted form of which hydrolyzes a variety of vasoactive peptides J. Biol. Chem. 274 (45), 32469-32477 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-UN-1999) International Center for Medical Research, Robe University School of Medicine, 7-5-1 Kusunoki, Chuo, Kobe
                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                          Raharjo, S.B., Nurhantari, Y., Saiki, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="soluble secreted endopeptidase delta"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Rammalia; Eutheria; Primates; Catarrhini; Hominid
1 (Dases 1 to 2636)
Jagerschmidt, A., Agnel, M. and Culouscou, J. M.
Three neprilysin-like membrane metallopeptidases
Patent: EP 1069188-A 3 17-JAN-2001;
SANOFI-SYNTHELABO (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 17.4; DB 10;
Pred. No. 5.2e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                         Ikeda,K., Emoto,N. and Matsuo,M. Direct Submission
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1. .2636
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                                                                                                                                      Tokoyama, M. and Matsuo, M.
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                         (bases 1 to 2601)
eda, K., Emoto, N., 1
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AF157106
AF157106.1 GI:6467400
                                                                               AF3U2075 2583 bp mRNA linear ROD 11-JUN-2001 Mns musculus neprilysin-like peptidase alpha mRNA, complete cds. AF302075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MVERAGWCRKKSPGFVEYGLMVLLLLLGAIVTLGVFYSIALRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain
Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saltama
351-0198, Japan
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                      Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan and phosphoramidon-sensitive endopeptidases J. Biol. Chem. 276 (24), 21895-21901 (2001)
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Pred. No. 5.1e+02;
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/db_xref="taxon:10090"
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Best Local Similarity 94.73
Matches 18; Conservative
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FEATURES

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AUTHORS TITLE

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JOURNAL MEDLINE PUBMED REFERENCE

PAT 30-MAY-2001

DEFINITION

RESULT 9 AF157106 LOCUS

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VERSION KEYWORDS

BASE COUNT ORIGIN

Gaps

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SRHIIYIDQPTLGMPSREYYENGGSNRKVREAYLOFWVSVATLLREDANLPRDSCLVO
EDMYQYLELEFQLAKATVPQEERHDVIALYHRMGLEELGSOFGLKGFDWTLFTOTVLZ
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RVNYRKALFGTMVEEVRWRECVGYVNSNMENAVGSLYVREAFPGDSKSMVRELIDKVR
                                                                                                                                                                                                               QPLLDILEVVGGWPVAMDRWNETVGLEWELERQLALMNSQFNRRVLIDLFIWNDDQNS
                                                                                                                                                                                                                                                                                                                                                                        MIYQYGNYSWDLADEQNVNGFNTLGENIADNGGVRQAYKAYLKWMAEGGKDQQLPGLD
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                                                                                                                                                                                                                                                                                                                                                    FFSKEQPQALNFGGIGMVIGHEITHGFDDNGRNFDKNGNNANDWWSNFSTQHFREQSEC
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/protein_id="AaG18447.1"
/db_xref="G1:10505362"
/translation="MVERAGWCRKKSPGFVEXGLMVLLLLLGAIVTLGVFYSIGKQL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
Bhirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
Iwatsubo, T. and Saido, T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42 most rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases
J. Biol. Chem. 276 (24), 21895-21901 (2001)
                                                                                                                                                       /translation="MGKSEGPVGMVESAGRAGOKRPGFLEGGLLLL
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                                                                         'note="unnamed protein product"
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Pred. No. 5.2e+02;
0; Mismatches 1;
                                                                                                                    /protein_id="CAC39975.1"
/db_xref="GI:14275326"
/organism="Homo sapiens'/db_xref="taxon:9606"
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Shirotani, K. and Saido, T.C.
Direct Submission
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FNWTLFIQNVLSSVEVELFPDEEVVVYGIPYLENLEDIIDSYSARTMQNYLVWRLVLD
                                                                                            RIGSLSQRFKEARVDYRKALYGTTVEEVRWRECVSYVNSNMESAVGSLYIKRAFSKDS
                                                                                                                                                    OIVFPAGILOPPFFSKOOPOSINFGGIGMVICHEITHGFDDNGRNFDKNGNMLDMWSN
FSARHRQOSOCMIYOYGNFSWELADNONVNGFSTLGBNIADNGGYRQAYKAYLKWLA
DGGRDORLPGLNLTYAQLFFINYAQVWCGSYRPFFAVOSIKTDVHSPLKYRVLGSLQN
QYACGGWLRHHVIPETNSRYSVFDILRDELEVILKGVLEDSTSOHRPAVEKAKTLYRS
CMNQSVIEKRDSEPLLSVLKMYGGWPVAMDKWNETMGLKWELERQLAVLNSOFNRRVI
                                     IDLEIWNDDQNSSRHVIYIDQPTLGMPSREYYFQEDNNHKVRKAYLEFMTSVATMLRK
                                                                                                               KSTVRELIEKIRSVFVDNLDELNWMDEESKKKAQEKAMNIREQIGYPDYILEDNNKHL
                                                                                                                                    DEEYSSLTFYEDLYFENGLQNLKNNAORSLKKLREKVDQNLW11GAAVVNAFYSPNRN
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2663)
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Pred. No. 5.2e+02;
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Pred. No. 5.2e+02;
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/db_xref="G1:14275328"
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/organism="Homo saplens'/db_xref="taxon:9606"
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1 Similarity 94.7%;
18; Conservative
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Best Local Similarity 94.7%;
Matches 18; Conservative
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/protein_id="CAC39974.1"
/db_xref="GI:14275324"
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Best Local Similarity 94.7%;
Matches 18; Conservative
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Mus musculus neprilysin-like peptidase gamma mRNA, complete cds.
AF302077
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Boileau, G. and Desgroseillers, L.

New metalloproteases of the neprilysin family

Patent: WO 0047750-A 14 17-ANG-2000;

BOILEAU GUY (CA); DESGROSEILLERS LUC (CA); UNIVERSTIE DE MONTREAL
                                                                                                        PAT 21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKWMAEGGKDQQLPGLDLTHEQLFFINYAQVWCGSYRPEFAIQSIKTDVHSPLKYRVI
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                   Euteleostomi;
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Shirotani, K., Tsubuki, S., Iwata, N., Takaki, Y., Harigaya, W.,
Maruyama, K., Kiryu-Seo, S., Kiyama, H., Iwata, H., Tomita, T.,
Iwatsubo, T. and Saido, T.C.
Neprilysin degrades both amyloid beta peptides 1-40 and 1-42
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Pred. No. 5.2e+02;
0; Mismatches 1;
                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                        'note-"unnamed protein product"
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                                                                                                           DNA
                                                                                                        2676 bp
Sequence 14 from Patent WO0047750.
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"/db_xref="taxon:9606"
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              2146 GTTCGCCATCCATCCATC 2164
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1 GTTCGCCATCCAGTCCATC 19
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illarity 94.7%;
Conservative 0
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Matches 18; Conserv
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GVRQAYKAYLRWLADGGKDQRLPGLNLFYAQLFFINYAQVWCGSYRPEFAVQSIKTDV
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1 (bases 1 to 2714)

Jagerschmidt,A., Agnel,M. and Culouscou,J.M.

Three neprilysin-like membrane metallopeptidases
Patent: EP 1069188-A 17-JAN-2001;
SANOFI-SYNTHELABO (FR)
                                                                                                                                                                                  Submitted (02-SEP-2000) Proteolytic Neuroscience Laboratory, Brain Science Instititute, RIKEN, 2-1 Hirosawa, Wako-shi, Saitama
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/protein_id="AAG18448.1"
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rapidly and efficiently among thiorphan- and phosphoramidon-sensitive endopeptidases J. Biol. Chem. 276 (24), 21895-21901 (2001)
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Pred. No. 5.2e+02;
0; Mismatches 1;
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/codon_start=1
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/db_xref="taxon:9606"
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Shirotani, R. and Saido, T.C.
Direct Submission
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/translation-"MGKSEGPYGMVESAGRAGOKRPGFLEGGLLLLLLUTAAALVALG
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DRAAVETERCHOSVJERKGSOPLLDILEVVGGWPVAADRWETVGENELER
OLALANSOFNRRVIDLETWNDDONSSHJITYIDOPTIGMPSREYTPNGGSNRKVER
XLQENNSVATLLEEDAMLPRDSCLVOEDMVOVLELETOLAKATVPOGERHDVIALTHR
MGLELCOSOGCIKGFDWTLFTOTVLSSVKIKLLDPGEVVYGIFYLQNLINITDTYSA
VGSLYYREAFPGEDSKSWYRELIDKVRTVFVETLDELGWMDESKKRAQEKAMSIREQI
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SSAKNUMDDWANGSTGLARERCROW"

2348. 2713

621 3'UTR BASE COUNT ORIGIN

Gaps ; 0 Length 2714; 1; Indels Ouery Match
91.6%; Score 17.4; DB 6;
Best Local Similarity 94.7%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 1;

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Search completed: July 8, 2003, 03:35:10 Job time: 211.093 secs

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Human prostate

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Human neprilysin-

Human SEP endopept

Human neprilysin-

Human SEP endopept Human soluble secr

neut nove

cDNA encoding

Human SEP CDNA inc

July

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Perfect score:

Sequence:

Scoring table:

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AAF89739
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AAF59660
AAF59661
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AAF59659
ABN84279
AAD28544
AAA63763
ABK48251
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AAF64428
AAA68155
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ABK75097
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 8, 2003, 00:43:28 ; Search time 119.376 Seconds (without alignments) 358.431 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                | SIDS2/goddata/geneseq/geneseqn-embl/NA1982.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl/NA1983.DAT:*
| SIDS2/goddata/geneseq/geneseqn-embl/NA1984.DAT:*
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       GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                                 2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               nucleic search, using sw model
                                                                                                                              1 gttcgccatccagtccatc 19
                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                  N_Geneseq_101002:*
                                                                                                      US-09-647-780A-20
19
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Maximum DB seq length: 2000000000
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Murine muscle ring Novel human polynu Pinus radiata PAL CDNA #386 encoding Bacillus lichenifo

Leukocyte immunogi Human cDNA sequenc

fucosyltrans Human cDNA encodin shear stress breast cance Human cDNA encodin

Human Human

Human

Human testicular

DNA encoding novel Human fucosyltrans

Human LIR-pbm36-2

Human cancer relat CDNA encoding nove

ALIGNMENTS

BP.

AAZ28826 standard; DNA; 19

RESULT 1

DAT: * DAT: *

/SIDS2/gcgdata/geneseq/genesegn-embl/NA1990 /gcgdata/geneseq/geneseqn-embl/NA1992

/gcgdata/geneseq/geneseqn-embl

/SIDS2

Post-processing:

Database

Total number of

Searched:

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA199

/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.

DAT:

.DAT:*

DAT: DAT:

AAZ28826;

Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; ss; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; probe; hybridsation. Rat membrane metalloprotease NEPII gene probe #16. 01-FEB-2000 (first entry) Synthetic. Rattus rattus. FR2777291-A1 15-OCT-1999.

08-APR-1998;

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

98FR-0004389

08-APR-1998;

ď, Bonhomme MC, Facchinetti Haret C, Gros C, Ouimet T, G Schwartz JC;

WPI; 1999-593429/51

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

/SIDS2/gcgdata/geneseg/genesegn-embl/NA2001A.DAT: /SIDS2/gcgdata/geneseg/genesegn-embl/NA2001B.DAT: /SIDS2/gcgdata/geneseg/genesegn-embl/NA2002.DAT:*

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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993 /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994

Human prostate exp Human prostate exp Human secreted pro Human prostate exp Human prostate exp Human secreted pro Human colon cancer Rat membrane metal Soluble secreted e Rat membrane metal Description ABV14605 - ABV05436 ABV05436 ABV44488 ABV44488 AAH26248 AAZ28826 AAZ28810 DB 324 340 569 569 1124 Length Query Score Result 8

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Disclosure; Fig 6; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-593429/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gros C,
                                                                                                                                                                                         Local Similarity
nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY44177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R2777291-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouimet T, G
Schwartz JC;
                                                                                                                                                                                                                                                                                                                                                          01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1999.
                                                                                                                                                                                                                                                                                                                                   AAZ28810;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                       RESULT 3
                                                                                                                                                                                                                                                                                                   AAZ28810
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                                                                                                                                                                                                                                                                                                                      # x 0 0 0 0 0 0 0 0 0 0 0 x 0
                                                                         Sequences AA228811-228827 represent probes for detecting the rat membrane metalloprotease designated neprilysine II (NEPII) gene (AA228810). NEPII is involved in (In)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII or for treatment of disorders related to peptidersic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic hypophyseal axis or endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase which is useful for treating sexual dysfunction, for e.g. male erectile dysfunction or female sexual dysfunction such as female sexual arousal disorder -
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted endopeptidase; SEP; endocrine; vasotropic; analgesic; enzyme; gynaecological; antisense-therapy; male erectile dysfunction; MED; female sexual dysfunction; FSD; female sexual arousal disorder; FSAD; premature ejaculation; anorgasmia; vaginismus; mouse; rat; ds.
                                                                                                                                                                                                                                                     Gaps
         New membrane metalloprotease NEP II, involved in proteolysis of neuronal and hormonal peptides, used to screen for inhibitors, potentially useful for treating e.g. cardlovascular disease
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                             Length 19;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wayman CP,
                                                                                                                                                                                                                                                                                                                                                                                                                            Soluble secreted endopeptidase (SEP) consensus DNA.
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/note= "Encodes catalytic domain"
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                                                                                                                                                                                                                            Score 19; DB 20;
Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wayman CP,
                                                                                                                                                                                                      Sequence 19 BP; 3 A; 8 C; 3 G; 5 T; 0 other;
                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1664..2286
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                                                                                                                                                                                                                                                                                                                                                        AAD28130 standard; DNA; 2286 BP.
                                                                                                                                                                                                                                                                                                1 GTTCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                         1 GTTCGCCATCCAGTCCATC 19
                                                      Page 24; 29pp; French.
                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%;
Matches 19; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-2001; 2001WO-IB01263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUL-2000; 2000GB-0017387.
                                                                                                                                                                                                                                                                                                                                                                                                     07-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stacey P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-155042/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PFIZ ) PFIZER LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200206492-A1
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misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harrow ID,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp.
                                                                                                                                                                                  disorders
                                                      Claim 3;
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                                                                                                                                                                                                                                                                                                                                  RESULT
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SEP consensus
                                                                                                                                                                                                                                      (e.g. female sexual arousal disorder (FSAD)). The SEP polypeptides are also useful for treating the above disorders and other disorders such as premature ejaculation, anorgasmia, sexual pain (e.g. vaginismus) and hypoactive sexual esire disorder. The present sequence is SEP consensus DNA sequence found in human, mouse and rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    designated neprilysine II (NEPII), which is involved in (in)activation of neuronal and hormonal peptide messengers. NEPII is used to screen for specific substrates (used to detect NEPII in cells and tissues) or inhibitors, which can also be used to detect NEPII in cells and tissues) or disorders related to peptidergic signalling in which NEPII in involved, e.g. cardiovascular or neurodegenerative diseases; growth disorders of endocrine origin; disturbances of the hypothalamic-hypophyseal axis or endocrine disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence represents the gene for the rat membrane metalloprotease
The invention relates to an isolated and/or purified nucleic acid encoding a human soluble secreted endopeptidase (SEP). The anti-SEP antibody and the compound which inhibits or selectively inhibits the human SEP protein are useful in the manufacture of a medicament for the prophylaxis and/or treatment of sexual dysfunction, in particular male erectile dysfunction (MED) or female sexual dysfunction (FSD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat; membrane metalloprotease; neprilysine II; NEPII; inactivation; neuron; hormone; peptide messenger; inhibitor; detection; disorder; cardiovascular disease; neurodegenerative disease; growth disorder; hypothalamic-hypophyseal axis; endocrine disorder; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0%; Score 19; DB 24; Length 2286; .0%; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonhomme MC, Facchinetti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2286 BP; 565 A; 601 C; 674 G; 446 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rat membrane metalloprotease NEPII gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2139 GTTCGCCATCCAGTCCATC 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haret C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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cytostatic; carcinogen; pharmacodyanamic marker;

gene; ss.

CDNA; 340 BP

X S

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expression marker cDNA 5427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                274 GTTCGCCATCCAATCCATC 292
         1 GITCGCCAICCAGICCAIC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-189862P.
2000US-207454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001WO-US05171
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2000US-219007P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-255281P
                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                     pharmacogenomic marker;
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                                                                                                                                                                ABV05436 standard;
                                                                                                                                                                                                                                                                                                    Human prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6-MAR-2000
                                                                                                                                                                                                       ABV05436;
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                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                 RESULT 5
ABV05436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e) selecting a composition for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assessing the prostate cell carcinogenic potential of a compound, determining whether prostate cancer has metastasized in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assessing the aggressiveness or indolence of prostate cancer in a
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monitoring the progression of prostate cancer in a patient, assessing the efficacy of a test compound to inhibit prostate
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                                                Length 2765;
                                                                                            Indels
684 A; 735 C; 787 G; 559 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 70 A; 101 C; 98 G; 55 T; 0 other;
                                                                                          ;
                                                DB 20;
                                                                   9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cDNA 14596.
                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 Match 91.6%; Score 17.4; I Local Similarity 94.7%; Pred. No. 47; es 18; Conservative 0; Mismatches
                                     100.0%; Score 19; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2438; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monahan JE;
                                                                                                                                                           2281 GTTCGCCATCCAGTCCATC 2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                 1 GTTCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                                           ABV14605 standard; cDNA; 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001WO-US05171.
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (b) monitoring the p(c) assessing the efcancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-662795/76.
                                                                Local Similarity
es 19; Conser
BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200160860-A2
  Seguence 2765
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13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .6-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schlegel R,
                                              Query Match
                                                                                                                                                                                                                                                                                                                                       ABV14605;
                                                                                   Matches
                                                                                                                                                                                                                                              RESULT 4
ABV14605
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Monahan JE;

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comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                   specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid molecule (I) coan nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 340 BP; 69 A; 109 C; 106 G; 56 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17.4; D)
Pred. No. 47;
0; Mismatches
                                                                                                                                                                                  Claim 1; Page 915; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 GITCGCCAICCAAICCAIC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GITCGCCATCCAGICCAIC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.6%;
llarity 94.7%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
'-hag 18; Conserve
WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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Gaps

1; Indels

DB 23; Length 324;

Ouery Match

Best Loca Matches

RESULT 6 ABV35683

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selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                         cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprise nucleotide sequence given in Tables 1-9 (ABW00010-ABW62213) of the a nucleotide sequence given in Tables 1-9 (ABW0001010-ABW62213) of the (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wovel isolated nucleic acid molecule associated with cancerous state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.4; DB 23; Length 569;
Pred. No. 49;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; human; HSIDD62; colon cancer; ovary cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 569 BP; 121 A; 166 C; 165 G; 116 T; 1 other;
                                     Human prostate expression marker cDNA 44479
                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein cDNA clone HSIDD62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 8827; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; human; HSIDD62; cc
tumour; diagnosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                             Human; prostate cancer; cytostati
pharmacogenomic marker; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 GTTCGCCATCCAATCCATC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTTCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH26248 standard; cDNA; 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.68;
94.78;
                                                                                                                                                                                                                                                                                                                                         2000US-207454P
2000US-211314P
                                                                                                                                                                                                                                                              20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                 2000US-219007P
2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2001 (first entry)
16-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                            40200160860-A2.
                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                 .8-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ma.
Local S. 18;
                                                                                                                                                                                                                                                                                                  17-FEB-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                              5-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                 39-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      schlegel R,
                                                                                                                                                                                                                      33-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH26248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (e)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH26248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                           Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23; Length 569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 569 BP; 121 A; 166 C; 165 G; 116 T; 1 other;
                                                                                                                                                           Human prostate expression marker cDNA 35674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 49;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.6%; Score 17.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 7417; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTCGCCATCCAATCCATC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTTCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВР
                                       ABV35683 standard; cDNA; 569 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABV44488 standard; cDNA; 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-207454P.
2000US-211314P.
2000US-219007P.
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                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-255281P
                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-662795/76
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tes 18; Conserv
                                                                                                                                                                                                                                                                                                      WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-DEC-2000;
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9-JUN-2000;
                                                                                                                   16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   6-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-MAY-2000;
                                                                                                                                                                                                                                                                                                                                              23-AUG-2001
                                                                           ABV35683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABV44488;
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RESULT 7
ABV44488
ID ABV4
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Homo sapiens

Key

26-JUL-2001

us-09-647-780a-20.rng

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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, adiagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P additionally. N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell of the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human colon cancer-associated polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for preventing, diagnosing and/or treating colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at time of publication, meaning no sequences are present for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention.
N.B. Pages 666 to 682 and page 7053 of the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.4;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 1027 to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 3574; 9803pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABV23433 standard; cDNA; 1746 BP
                                                                                                                                                                                                                                                                                                                                                                          Barash SC, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GITCGCCATCCAGICCAIC 19
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Local Similarity 94.7%;
Les 18; Conservative 0
                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                   990S-0157137
990S-0163280
                                                                                                                                    28-SEP-2000; 2000WO-US26524
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                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI: 2001-235357/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAG75602.
WO200122920-A2.
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                                                                                                                                                                                                   29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-AUG-2001.
                                                                  05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                          Ruben SM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iluretic and hypotensive activities. Vectors, host cells, intibodies, recombinant methods for producing the secreted protein, and screening methods are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotides, translation products and antibodies corresponding to this gene could be useful in the diagnosis, detection and/or treatment of diseases and/or disorders of the gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ystem, as well as colon tumours and ovarian cancer. Antagonists lirected against the gene translation product may be useful in prohibiting or eliminating its biological activities, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's diseases and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of cDNA clone HSIDD62 (deposited as AAB82595), which encodes a novel human secreted protein (see binding protein (ANPBP), which is thought to have duretic protein (ANPBP), which is thought to have duretic (particularly natriuretic) and hypotensive activities. The gene tax expressed in adult small intestine tissue as well as in colon distribution and homology to human ANPBP indicate that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 1124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon cancer antigen encoding cDNA SEQ ID NO: 2089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 17.4;
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1(a); Page 330; 339pp; English.
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH35007 standard; cDNA; 1226 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTTCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-2001; 2001WO-US01436:
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                                                                                                                                 2..367
/*tag= a
/partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 94.7 hes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colorectal carcinoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483137/52
P-PSDB; AAB82596..
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Homo sapiens

Human;

AAH35007;

Query Match

Matches

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Gaps

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Homo sapiens
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                                                                                                                                                                                                                                                                     patient;
                                                                                                                                                                                                                                                                                                                                         Matches
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  g
                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention relates to an isolated nucleic acid molecule. (1) comprising
                                                                                                                                                                                                                                                                                     selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                    assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                     a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                        I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                               Score 17.4; DB 23; Length 1746; Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                           Sequence 1746 BP; 299 A; 531 C; 580 G; 336 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 29281.
                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                        Claim 1; Page 4269; 11750pp; English
                                                                                          Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV29290 standard; cDNA; 1746 BP
                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTTCGCCATCCAGTCCATC 19
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2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                              91.6%;
llarity 94.7%;
Conservative
                    2000US-207454P
                            2000US-211314P.
2000US-219007P.
                                                2000US-255281P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                          Endege WO,
                                                                                                                                                                                                                                                       cancer in a patient;
                                                                                                            WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
ses 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200160860-A2.
                                                                                                                                                                                                                                                                            a patient;
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09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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                   5-MAY-2000;
                            09-JUN-2000;
                                                13-DEC-2000;
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                                                                                        Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV29290;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                               patient;
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Matches
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comprising

(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                   prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metalloprotease, IGS5, infection, pain, cancer; diabetes; obesity; anorexia; bulmia; asthma; Parkinson's disease, acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer; allergy; benign prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple sclerosis; alzheimer's disease; neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subarachnoid hemorrhage; cerebral ischemia; cerebral infarction; peripheral vascular disease; Raynaud's disease; motility disorder; gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tummour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia; Huntington's disease; gilles de la Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule (I) companies of the nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1746 BP; 299 A; 531 C; 580 G; 336 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17.4; DE
Pred. No. 54;
0; Mismatches
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 6257; 11750pp; English.
                                                                                       Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 GTTCGCCATCCAATCCATC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF89737 standard; DNA; 2076 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GITCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 91.6%;
Local Similarity 94.7%;
es 18; Conservative
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                                                                                       Endege WO,
                                                                                                                                                                      WPI; 2001-662795/76
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                                                                                       Schlegel R,
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"metalloprotease enzyme IGS5"

/rtag= a /product= '

Location/Qualifiers 1..2076

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Trinary retention, osteoporosis, angina pectoris, myocardial infarction, troke, ulcers, allergies, benign prostatic hypertrophy, migraine, sychotic and neurological disorders, autism, multiple sclerosis, lisheimer's disease, and other neurodegenerative diseases, sleep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastric emptying, post-operative or diabetic gastroparesis, diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a human metalloprotease enzyme designated (GS5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, parkinson's disease, acute heart failure, hypotension, hypertension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral
infarction, peripheral vascular disease, Raynaud's disease, kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                             New IGS5 polypeptides useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular diseases, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2076 BP; 493 A; 578 C; 636 G; 369 T; 0 other;
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Pred. No. 55;
0; Mismatches
                                                                                                                                                                                                                                                    Weske M;
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 5-6; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1926 GTTCGCCATCCAATCCATC 1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GITCGCCATCCAGICCATC 19
                                                                                                                                                                                                                                                  Deleersnijder W, Wiegers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.6%;
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                  99NL-1013616.
2000EP-0201937.
                                                                         17-NOV-2000; 2000WO-EP11532
                                                                                                                                                                      2000NL-1015356
                                                                                                                                                                                                            (SOLV ) SOLVAY PHARM BV
                                                                                                                                                                                                                                                                                   WPI; 2001-343815/36.
P-PSDB; AAB83840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isorder, epilepsy,
 WO200136610-A1
                                                                                                                                                                      31-MAY-2000;
                                                                                                                 .9-NOV-1999;
                                                                                                                                9-NOV-1999;
                                                                                                                                                    -MAY-2000;
                                     25-MAY-2001
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The invention relates to an isolated, enriched, or purified protease polypeptide (I) and polynucleotide (II) encoding (I). (I) may be used to screen for substances (S) that may modulate its activity. Administering 8 (which modulates protease activity in vice of 10 may be used to treat a disease or disorder selected from cancers (e.g., of tissues, of blood or haematopoletic origin, of the breast, colon, lung, prostrate, cervical, brain, ovarian, bladder or kidney), immune-related diseases and disorders; cardiovascular disease, brain or neuronal-associated diseases (e.g., central or peripheral nervous system diseases, migraine, pain, sexual dysfunction, mood disorders, attention disorders, cognition

Novel protease polypeptide useful for screening for substances that may be used to treat, e.g., cancers, immune-related diseases, e.g., cancers, e.g., psychotic and inflammatory

Claim 30; Figure 1R-S; 232pp; English

disorders

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Manning G,

Sudarsanam S,

Whyte D,

Plowman GD,

Payne V;

WPI; 2002-041502/05.

P-PSDB; AAU72903.

04-MAY-2000; 2000US-201879P.

(SUGE-) SUGEN INC

34-MAY-2001; 2001WO-US14431.

WO200183782-A2. Homo sapiens.

08-NOV-2001

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disorders, hypotension, hypertension, psychotic disorders, neurological disorders and dyskinesias), metabolic disorders and inflammatory disorders. (I) may also be useful as a diagnostic tool for a disease or disorder such as those above. AAS97159-AAS97195 represent human protease coding sequences and primers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metalloprotease; IGS5; infection; pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial inarction; stroke; ulcer; allergy; bendgn prostatic hypertrophy; migraine; psychotic disorder; neurological disorder; autism; multiple sclerosis; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disease; sleep disorder; epilepsy; kidney disease; cardiovascular disease; arteriosclerosis; cerebrovasospasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        emia; cerebral infarction;
disease; motility disorder,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a human metalloprotease enzyme IGS5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2232 BP; 512 A; 620 C; 705 G; 395 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ischemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17.4; E
Pred. No. 56;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raynaud's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2082 GITCGCCATCCAATCCATC 2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subarachnoid hemorrhage; cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GITCGCCATCCAGICCAIC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF89739 standard; DNA; 2262 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 94.78;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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andrectic; antiinflammatory; aspartyl protease; cysteine protease; metalloprotease; serine protease; cancer: haematopoietic; breast; colon; lung; prostrate; cervical; brain; ovarian; bladder; kidney; pain;

.mmune-related disease; cardiovascular disease; neuronal disease;

migraine; sexual dysfunction; mood disorder; attention disorder, cognition disorder; hypotension; hypertension; psychotic disordedyskinesia; metabolic disorder; inflammatory disorder; ss.

lypertension; psychotic disorder

Human; protease; PCR primer; cytostatic; immunomodulator; cardiant; vasotropic; antimigraine; analgesic; endocrine; nootropic; tranquiliser; hypertensive; hypotensive; neuroleptic; neuroprotective; anabolic;

Human metalloprotease partial DNA sequence #15.

26-FEB-2002 (first entry)

AAS97186;

AAS97186 standard; cDNA; 2232 BP

RESULT 13 AAS97186 Human protease, PRTS-13 cDNA.

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ids5. IGS5 polynucleotides and polypeptides are useful for treating infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, ParkInson's disease, acute heart failure, hypotension, hypertension, uninary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, allergies, benign prostatic hypertrophy, migraine, psychotic and neurological disorders, autism, multiple sclerosis, Alzheimer's disease, and other neurodegenerative diseases, sleep disorder, epilepsy, cardiovascular diseases, arteriosclerosis, cerebrovasospasm, subarachnoid hemorrhage, cerebral ischemia, cerebral infarction, peripheral vascular disease, Raynaud's disease, kidney diseases, gastrointestinal disorders, motility disorders and conditions of delayed gastroparestis, of delayed gastroparestis,
  gastrointestinal disorder; gastric emptying; gastroparesis; diarrhoea; inflammation; chemotherapy induced injury; tumour invasion; immune disorder; arthritis; endotoxin shock; sepsis; diabetes mellitus; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diarrhoea, inflammations, chemotherapy induced injury, tumour invasion, immune disorders, arthritis, endotoxin shock, sepsis, complications of diabetes mellitus, and severe mental retardation and dyskinesias, such as Huntington's disease or Gilles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes a human metalloprotease enzyme designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
91.6%; Score 17.4; DB 22; Length 2262;
Best Local Similarity 94.7%; Pred. No. 56;
Matches 18; Conservative 0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New IGS5 polypeptides useful for treating infections, pain, cdiabetes, obesity, anorexia, bulimia, asthma, schizophrenia, hypertension, urinary retention and Parkinson's disease
                                                                                                                                                                  Location/Qualifiers
1..256.7
/*iag= a
/product= "metalloprotease enzyme IGS5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weske M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 8-9; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deleersnijder W, Wiegers R,
                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1999; 99EP-0203862.
19-NOV-1999; 99NL-1013616.
31-MAY-2000; 2000EP-0201937.
31-MAY-2000; 2000NL-1015356.
                                                                                                                                                                                                                                                                                                                                                            2000WO-EP11532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-343815/36.
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                                                                                                                              Homo sapiens
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                                                                                     Gilles
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Gaps
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2112 GTTCGCCATCCAATCCATC 2130

1 GTTCGCCATCCAGTCCATC 19

ô a AAD30580 standard; cDNA; 2318 BP

RESULT 15 AAD30580 21-MAY-2002

AAD30580;

AXXXX

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The invention relates to an isolated human protease polypeptide (PRTS).

PRTS protein and DNA are useful for diagnosing, treating and preventing gastrointestinal disorders (gastriis, cirrhom's disease),

anomia, asthma), cardiovascular disorder (atherosclerosis, hypertension, myocardial infarction), cell proliferative disorders (hepatitis, cancer, psoriasis), developmental disorders (Cushing's syndrome, hypothyroidism), epithelial disorder (vitiligo, keloid, eczema), neurological disorders (epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, protein is useful in a number of dung screening techniques and to analyse the proteome of a tissue or cell type. PRTS DNA is useful for creating knockin humanised animals or transgenic animals to model human cathing subsection the protein germline gene therapy and in microarrays utilising fluids or tissues from patients to detect altered PKIN expression. The present sequence is human PRTS-13 CDNA.
                                               Human, protease, PRTS-13; enzyme, gastritis, cirrhosis, Crohn's disease; gastrointestinal disorder; autoimmune; inflammatory, cell proliferative; cardiovascular; developmental; epithelial; neurological; reproductive; AIDS; Acquired Immune Deficiency Syndrome; allergy; rheumatoid arthritis; anaemia; asthma; atherosclerosis; hypertension; myocardial infarction;
                                                                                                                               hepatitis, cancer; psoriaais; Cushing's syndrome; hypothyroidism; eczema; epilepsy; Alzheimer's disease; Huntington's disease; Parkinson's disease; Pick's disease; infertility; vitiligo; drug screening; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment of gastrointestinal, cardiovascular, autoimmune/Inflammatory, cell proliferative, developmental, epithelial and neurological disorders
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Ramkumar J, Yang J;
Borowsky ML;
Lal P, Lee S, Todd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I AR, Hafalia AJA, Lu DAM, re, Kaliick DA, Nguyen DB, Lee Griffin JA, Policky JL, Ramk L, Rearney L, Baughn MR, Bor MG, Burford N; Walla NK, Lal MG, Lu Y;
                                                                                                                                                                                                                                                                                                                                                                         /product= "Mature PRTS-13 protein'
                                                                                                                                                                                                                                                                                    "Human PRTS-13 protein
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Thangavelu K, Ding L, Kearney L, Baughn
Sanjamwala MS, Yao MG, Burford N; Walla
Lo TP, Tang YT, Elliott VS, Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Page 174-175; 182pp; English.
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-225988P
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428..1648
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Das D, Ka
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Tribouley CM,
                                                                                                                                                                                                      Homo sapiens.
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28-JUL-2000;
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SQ Sequence 2318 BP; 526 A; 647 C; 735 G; 410 T; 0 other;

Gaps Query Match
91.6%; Score 17.4; DB 24; Length 2318;
Best Local Similarity 94.7%; Pred. No. 56;
Matches 18; Conservative 0; Mismatches 1; Indels 0;

Search completed: July 8, 2003, 02:19:14 Job time: 120.376 secs g

2565, Ap 7, Appli 7, Appli

Appl Appli Appli Appl Appl

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S-03-101-402-11.
S-03-101-402-11.
Patent No. 6384203
GENERAL INFORMATION:
APPLICANT: Cosman, David J.
APPLICANT: Anderson, Dirk M.
APPLICANT: Borges, Luis
TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobul
TITLE OF INVENTION: Like Receptors (LIR)
                                                                           Sequence 1, Appli
Sequence 70, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 26, Appli
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Sequence
Sequence
Sequence
                                       Sequence
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TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Maderials and Methods for the
TITLE OF INVENTION: Maddication of Plant Lignin Content
FILE REPERENCE: 10000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07.12
PRIOR PILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-10-11
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR PILING DATE: 1996-09-11
PRIOR PILING DATE: 1998-10-09
PRIOR PILING DATE: 1998-10-09
PRIOR PILING DATE: 1998-10-09
PRIOR PILING DATE: 1998-10-09
SEQ ID NOS: 405
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LENGREN PRIOR PRI
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US-08-824-692-25
US-09-134-001C-2565
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· US-09-077-354B-3

US-08-824-692-26

US-08-824-692-28
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PCT-US95-07536-9
US-09-091-899-9
US-09-040-774-1
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PCT-US95-06420-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.8;
Pred. No. 5
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APPLICATION NUMBER: 08/842,248
FILING DATE: 1997-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 248, Application US/09615192A Patent No. 6410718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.2%;
89.5%;
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Best Local Similarity 89.5
Matches 17, Conservative
                                                                                                               5410
6048.
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ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 2624-A
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222.151 Million cell updates/sec
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Sequence 58,
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Sequence 11,
Sequence 2,
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Seguence 17
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'cgn2_6/ptodata/1/ina/5A_COMB.seq:*
'cgn2_6/ptodata/1/ina/5B_COMB.seq:*
'cgn2_6/ptodata/1/ina/6A_COMB.seq:*
'cgn2_6/ptodata/1/ina/RB_COMB.seq:*
'cgn2_6/ptodata/1/ina/RCTUS_COMB.seq:*
'cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
'cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-928-213B-58
US-08-459-586-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-459-586-11
US-08-282-696-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441362 seqs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-031-563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                           - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gttcgccatccagtccatc 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                          US-09-647-780A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
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Score

Result

Post-processing:

Database.

Potal number of

Searched:

Scoring table:

Perfect score:

Title:

Sequence:

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Run

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Gaps

GLYCOSIDASE ENZYMES 72

416 GTTCCCCATCCCGTCCATC 434

PatentIn Ver. 2.0

NUMBER OF SEQ ID NOS:

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APPLICANT: Allen, Steve
APPLICANT: Anderson, Shawn
APPLICANT: Falco, Carl
APPLICANT: Ralos, Carl
APPLICANT: Ralos, Trailski, Antoni
TITLE OF INVENTION: Genese Encoding Sulfate Assimilation Proteins
FILE REFERENCE: BB-1167-A
                                                                                                                                                                                                              E: Gray Cary Ware & Freidenrich LLP 4365 Executive Drive, Suite 1600
                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Windows95.
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,078
FILING DATE: 13-MUG-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/949,026
FILING DATE: 10.0CT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09346408B Patent No. 6338966
GENERAL INFORMATION:
                                                                                Sequence 58, Application US/09134078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TICGCCATCCAGICCAI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 81.1%;
1 Similarity 94.1%;
16; Conservative
                                                                                                              GENERAL INFORMATION:
APPLICAMT: BYLINA, Edward
TITLE OF INVENTION: GLYCOS
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2055 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               858/677-1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: · linear
                                                                                                                                                                                                                                                    San Diego
                                                                                                                                                                                                                                                                                           USA
                                                                                              Patent No. 6368844
                                                                                                                                                                                                              ADDRESSEE:
STREET: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                         RESULT 4
US-09-134-078-58
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US-09-134-078-58
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US-09-346-408-3
                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Family of Immunoregulators Designated Leukocyte Immunoglobulin-Like Receptors (LIR)
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                                                                                                                                                                                           Length 2446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 2446;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Janis C. Henry, Immunex Corporation 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                             DB 4;
                                                                                                                                                                                         Score 15.8; DE
Pred. No. 67;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.2%; Score 15.8; Best Local Similarity 89.5%; Pred. No. 6: Matches 17; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
OPERATING SYSTEM: Microsoft Word 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,248A
FILIAD DATE: April 24, 1997
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08842248A Patent No. 6448035
                                                                                                                                                                                                                                                                                       416 GTTCCCCATCCCGTCCATC 434
                                                                                                                                                                                                                                                                  1 GTTCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cosman, David J.
TITLE OF INVENTION: Family of
TITLE OF INVENTION: Leukocyte
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELECOMMUNICATION INFORMATION
                                                                                                                                                                                       Query Match 83.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 587-04
(206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
171..1037
                                                                                                            ) NAME/KEY: CDS
; LOCATION: (171)...(1040)
US-09-310-463-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                        ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 98101
SOFTWARE: Pater
SEQ ID NO 11
LENGTH: 2446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-842-248A-11
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE:
                                                         TYPE: DNA
                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                              RESULT 3
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Gaps

; DB 4; Length 2055; 1e+02; Indels

Pred. No. 1e+0 ; Mismatches

CURRENT APPLICATION NUMBER: US/09/346,408B CURRENT FILING DATE: 1999-07-01

Gaps

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Cytomegalovirus Gene Region Involved in Down-Regulation o MHC Class I Heavy Chain Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jones, Thomas R.
APPLICANT: Campbell, Ann E.
TITLE OF INVENTION: Identification of a Human
TITLE OF INVENTION: Cytomegalovirus Gene Region Involved in Down-Regulation c
TITLE OF INVENTION: MHC Class I Heavy Chain Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 14.8; DB 1;
Pred. No. 1.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                              American Cyanamid Company
                                                                            GENERAL INFORMATION:
APPLICANT: Jones, Thomas R.
APPLICANT: -Campbell, Ann E.
TITLE OF INVENTION: Identification of
TITLE OF INVENTION: Cytomegalovirus Gr
TITLE OF INVENTION: AMC Class I Heavy
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,425-01
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/08282696 Patent No. 5846806 GENERAL INFORMATION:
                                      Sequence 17, Application US/08459586 Patent No. 5720957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                845 GIGCGCCTICCAGICCAI 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barnhard, Elizabeth M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTTCGCCATCCAGTCCAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.9%;
88.9%;
                                                                                                                                                                                                                                                                   One Campus Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1174 base pairs
                                                                                                                                                                                                                                                                                                            New Jersey
United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XY: United States 07470-8426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEOUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 77.9
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201-683-4117
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                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: American
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                      Parsippany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wayne
                                                                                                                                                                                                                                                                                                                                                07054
RESULT 7
US-08-459-586-17
                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-282-696-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                0
                                                                                                                                                                                                        Score 15.4; DB 4; Length 2280; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seville, Mark
Cull, Millard G.
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,213B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.9%; Score 15; DB 4; Le
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: ENZYCO-02550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESCRIPTION: /desc = "DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL,
  EARLIER APPLICATION NUMBER: 60/092,833
EARLIER FILING DATE: July 14, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 58, Application US/08928213B Patent No. 6238905
GENERAL INFORMATION:
APPLICANT: MCHenry, Charles S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-Sep-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOLOENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1109 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ 1D NO: 58: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            825 TTCGCAATCCAGTCCAT 841
                                                                                                                                                                                                                                                                                      2 TTCGCCATCCAGTCCAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: CA
                                                                                                                       ; TYPE: DNA
; ORGANISM: Momordica charantia
US-09-346-408-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCGCCATCCAGTCCA 701
                                                                                                                                                                                                        Query Match 81.1%;
Best Local Similarity 94.1%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 TCGCCATCCAGTCCA 17
                                      NUMBER OF SEQ ID NOS: 12
SOFTWARE: Microsoft Office 97
SEQ ID NO 3
LENGTH: 2280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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Best Local Similarity
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Gaps

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Gaps

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APPLICANT: Jones, Thomas R.
APPLICANT: Campbell, Ann E.
TITLE OF INVENTION: Identification of a Human
TITLE OF INVENTION: Cytomegalovirus Gene Region Involved in Down-Regulation of
TITLE OF INVENTION: MHC Class I Heavy Chain Expression
Length 1328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hemker, Michael;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crueger, Anneliese; Dellweg, Hans-Georg; Lenz,
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stratmann, Ansgar
TITLE OF INVENTION: PROCESSES FOR PREPARING ACARVIOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jurgen; Schroder, Werner; Pape, Hermann;
Goeke, Klaus; Schaper, Beate; Hemker, Mi
Piepersberg, Wolfgang; Distler, Jurgen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURLICATION NUMBER: US/08/282,696
FILING DATE: 29-JUL-1994
      Score 14.8; DB 1;
Pred. No. 1.9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , DB 2;
1.9e+02;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 14.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
BDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     Sequence 11, Application US/08282696
Patent No. 5846806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08816105A Patent No. 5989882
                                                                                                               642 GTGCGCCTTCCAGTCCAT 659
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                                                                                       1 GTTCGCCATCCAGT 18
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NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 201-831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic) US-08-282-696-11
      77.9%;
ilarity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.9%;
ilarity 88.9%;
Conservative
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LENGTH: 1328 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201-831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 16; Conserva
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        Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                              RESULT 10
US-08-282-696-11
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APPLICANT: Jones R.
APPLICANT: Campbell, Ann E.
TITLE OF INVENTION: Identification of a Human
TITLE OF INVENTION: Cytomegalovirus Gene Region Involved in Down-Regulation of
TITLE OF INVENTION: MHC Class I Heavy Chain Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version.#1:30
CUBRENT APPLICATION DATA:
BELLCATION NUMBER: US/08/459,586
FILING DATE: 02-JUN-1995
          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14.8; DB 2;
Pred. No. 1.8e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   American Cyanamid Company
                                  омыек: US/08/282,696
29-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08459586 Patent No. 5720957
                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    845 GIGCGCCTICCAGTCCAT 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTTCGCCATCCAGTCCAT 18
                                                                                                                                                   31,088
                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
TELEFAX: 201-831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match. 77.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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:: New Jersey
:RY: United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   LENGTH: 1174 base pairs
                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                single
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2/CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
|S-08-459-586-11
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                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                        US-08-282-696-17
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US-08-459-586-11
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Score 14.8; DB 3; Length 4880;
Pred. No. 2.1e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; DB 4;
2.1e+02;
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Pred. No. 2.1e+
0; Mismatches
                                                                                                                                                                                                                  Sequence 1, Application US/09392277A
Patent No. 6451977
GENERAL INFORMATION:
APPLICANT: Frederic de Sauvage
APPLICANT: Arnon Rosenthal
TITLE OF INVENTION: Fused
FILE REFERENCE: PL27ER1P1
CURRENT PPLICATION NUMBER: US/09/392,277A
CURRENT FILING DATE: 1999-09-03
EARLIER APPLICATION NUMBER: US 09/258,000
EARLIER PPLICATION NUMBER: US 09/258,000
EARLIER FILING DATE: 1999-02-25
EARLIER FILING DATE: 1999-02-26
NUMBER: OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: P1272.
CURRENT APPLICATION NUMBER: US/09/031,563A
CURRENT FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-031-563-4
; Sequence 4, Application US/09031563A
; Patent No. 6022708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2866 TTCGCTATCCAGTCCACC 2883
                                                                                                            2866 TTCGCTATCCAGTCCACC 2883
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                                                                                   2 TTCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ITCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Frederic de Sauvage
APPLICANT: Arnon Roshenthal
TITLE OF INVENTION: Fused
        77.9%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 77.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: unknown N
LOCATION: 4160, 4243, 4361
; OTHER INFORMATION: unknown
US-09-392-277-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 88.9
Matches 16; Conservative
      Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-031-563-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 5125
                                                                                                                                                                                                       -09-392-277-1
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US-09-392-277-4
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2e+02;
    TRANSFERASE AND FOR USING IT IN THE CONVERSION OF ACARBOSE HOMOLOGUES INTO ACARBOSE, FOR THE PREPARATION OF ACARBOSE HOMOLOGUES
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
                                                                                                                          ADDRESSEE: Sprung Kramer Schaefer & Briscoe STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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APPLICANT: Arnon Roshenthal
TITLE OF INVENTION: Fused
FILE REFERNCE: P1272
CURRENT APPLICATION NUMBER: US/09/031,563A
CURRENT FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,105A
FILING DATE: 14-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19625269.5
FILING DATE: 25-JUN-1996
RICHA PAPLICATION DATA:
APPLICATION NUMBER: DE 19611252.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: DE 19611252.4
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09031563A Patent No. 6022708
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                                                                                                                                                                                                                                                                                                           SYSTEM: System 7.5
WordPerfect 3.5
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                                                                                                                                                                                                                                                                                       Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.9%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: 4160, 4243, 4361
; OTHER INFORMATION: unknown
US-09-031-563-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                          10591-5144
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                                                                                                                                                                                                         USA
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0; Gaps
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77.9%; Score 14.8; DB 4; Length 5125;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0;
                                   GENERAL INFORMATION:
APPLICANT: Frederic de Sauvage
APPLICANT: Frederic de Sauvage
APPLICANT: Arnon Rosenthal
TITLE OF INVENTION: Fused
FILE REFERENCE: P1272R1P1
CURRENT APPLICATION NUMBER: U$/09/392,277A
CURRENT APPLICATION NUMBER: U$ 09/258,000
EARLIER APPLICATION NUMBER: U$ 06/076,072
EARLIER FILING DATE: 1999-02-25
EARLIER FILING DATE: 1999-02-25
NUMBER OF SEQ ID NOS: 28
LENGTH: 5125
TYPE: DNA
ORGANISM: Homo sapiens
US-09-392-277-4
Sequence 4, Application US/09392277A Patent No. 6451977
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Search completed: July 8, 2003, 09:32:42 Job time: 27.2793 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 8, 2003, 19:09:54; Search time 109.737 Seconds

(without alignments)

273.390 Million cell updates/sec

Title: US-09-647-780A-20

Perfect score: 19
Sequence: 1 gttcgccatccagtccatc 19
Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1105431 seqs, 789497651 residues

Total number of hits satisfying chosen parameters: 2210862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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10: /cgn2_6/ptcdata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptcdata/2/pubpna/US10_NEW_LUBb.seq:*
12: /cgn2_6/ptcdata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptcdata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptcdata/2/pubpna/US60_PUBCOMB.seq:*
Pred. No. is the number of results predicted by chance to have

oubpna/US07_PUBCOMB.seq oubpna/US08_NEW_PUB.seq oubpna/US08_PUBCOMB.seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_NA

Database :

ubpna/US09_NEW_PUB.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

			-		SUMMARIES		
Result No.	Score	Query Match	å Duery Match Length 1	DB	QI QI	Description	
. [17.4	91.6	1226	. 6	US-10-106-698-2099	Sequence 2099, Ap	
14	3 17.4	91.6	2893	5	US-10-017-273A-4	Sequence 4, Appli	
(*)	3 17.4	91.6	2893	10	US-09-905-846-1	Sequence 1, Appli	
4	17.4	91.6	2975	σ	US-10-017-273A-5	Sequence 5, Appli	
4)	5 17.4	91.6	2975	10	US-09-905-846-5	Sequence 5, Appli	
T.	5 16.4	86.3	1431	10	US-09-908-988B-1	Sequence 1, Appli	
0	16	84.2	558	6	US-10-156-761-4649	Sequence 4649, Ap	
ņ	3 16	84.2	9025608	6	US-10-156-761-1	Sequence 1, Appli	
Ü	15.8	83.2	477	6	US-09-918-995-2051	Sequence 2051, Ap	
10	15.8.	83.2	548	10	US-09-815-343-386	Sequence 386, App	
c 11	15.8	83.2	642	10	US-09-974-300-2388	Sequence 2388, Ap	
12	15.8	83.2	1194	σ	US-10-156-761-5444	Sequence 5444, Ap	
c 13	3 15.8	83.2	1479	6	US-09-844-948-3	Sequence 3, Appli	
14	15.8	83.2	2446	6	US-10-139-662-11	Π	
15	15.8	83.2	2446	6	US-10-139-683-11	Sequence 11, Appl	
c 16	15.8	83.2	2557	σ	US-09-844-948-1	Sequence 1, Appli	
17	15.8	83.2	3583	σ	US-10-084-817-202	20	
C 18	15.8	- 83.2	10115	6	US-09-764-891-7941	Sequence 7941, Ap	
19	15.8	83.2	9025608	σ	US-10-156-761-1	Segmence 1. Appli	

Sequence 58, Appl Sequence 58, Appl Sequence 1418, Ap Sequence 17150, A Sequence 17150, A	Sequence 337, App Sequence 4106, Ap Sequence 900, App Sequence 7326, Ap	Sequence 32026, A Sequence 32021, A Sequence 12229, A Sequence 12229, A	<u>~</u>	Sequence 0011, Ap Sequence 963, App Sequence 10290, A Sequence 3666, Ap Sequence 413, App	Sequence 11, Appl Sequence 1718, Ap Sequence 1718, Ap Sequence 5011, Ap
US-10-121-032-58 US-10-093-037-58 US-09-917-800A-1418 US-09-864-761-17150 US-09-960-352-446	US-10-156-761-337 US-10-156-761-4106 US-09-563-817-900 US-10-156-761-7326	US-09-918-995-32026 US-09-918-995-32021 US-09-918-995-12229 US-09-770-149-408	US-09-910-943-253 US-10-118-495-1 US-09-822-830A-469 US-10-128-714-7011	US-10-128 / 14-2011 US-09-974-300-963 US-10-198-846-10290 US-09-880-107-3666 US-09-070-927A-413	US-10-128-714-11 US-10-092-154-1718 US-09-764-847-1718 US-10-128-714-5011
2055 9 2055 9 2055 9 10 152 10 224 10	445 10 1533 9 330 10 387 9	447 9 456 9 466 9	707 10 1252 9 1413 10 1458 9	1941 10 2000 9 2209 10 2760 10	1275 9 1301 9 1301 10 1513 9
	78.9 15 77.9 3			•	
15.4 81 15.4 81 15.4 81 15 78	15 78 15 78 14.8 77	14.8 77 14.8 77 14.8 77	14.8 77 14.8 77 14.8 77	14.8 77 14.8 77 14.8 77 14.8 77	14.8 77 14.8 77 14.8 77 14.8 77
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ALIGNMENTS

RESULT 1

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	13-101-106-698-2099	
	Sequence 2099, Application US/10106698	
	; Publication No. US20030109690A1	
	; GENERAL INFORMATION:	
		s and
	; FILE REFERENCE: PA005P1	
	APPLICATION N	
	; CURRENT FILING DATE: 2002-03-27	
	APPLICATION N	
	FILING DATE	
	APPLICATION N	
	II.	
	SEQ ID NOS: 85	
	; SOFTWARE: PatentIn Ver. 3.0	
	; SEQ ID NO 2099	
	; LENGTH: 1226	
	; TYPE: DNA	
	; ORGANISM: Homo sapiens	
•	FEATURE:	
	; NAME/KEY: misc_feature	•
	; LOCATION: (164)(164)	
	; OTHER INFORMATION: n equals a,t,g, or c	
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	ON: (1180)(
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	COUNTRY INDOMANTON: CANADA + CONT.	
	EX. misc feature	
	; OTHER INFORMATION: n equals a,t,g, or c	
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APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
TITLE OF INVENTION: Compounds for the treatment of sexual dysfunction
FILE REFERENCE: PCS10926APME
                                                                                         Length 2893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 2975;
                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Naylor, Alasdair M.
Van Der Graaf, Pieter H
Wayman, Christopher P.
Wayman: Treatment of Male Sexual Dysfunction
NCE: PC22013
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CURRENT FILING DATE: 2001-07-13
PRICA APPLICATION NUMBER: 0017387.2
PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/017,273A
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NUMBER: US 09/905,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NT FILING DATE: 2001-12-12 APPLICATION NUMBER: US 60/265,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ING DATE: 2001-04-06
LICATION NUMBER: GB 0120679.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 0030647.2
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                                                                                                                                                                                           1 GTTCGCCATCCAGTCCATC 19
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Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                            Query Match 91.6%;
Best Local Similarity 94.7%;
Matches 18; Conservative
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                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-905-846-5
                        ; ORGANISM: Ho
US-09-905-846-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 5
LENGTH: 29
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Roderick Thomas Walsh (1998) Applicant of sexual dysfunction ILE REFERENCE: PCS10926APME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 2893;
  Length 1226;
                                                                                                                                                                                                                                                                                                                                                               PLICANT: Naylor, Alasdair M.
PLICANT: Van Der Graaf, Pieter H
PLICANT: Christopher P.
TLE OF INVENTION: Treatment of Male Sexual Dysfunction
    DB 9;
                                                    0; Mismatches
Score 17.4;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 17.4;
Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRENT APPLICATION NUMBER: US/10/017,273A
RRENT FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 0017387.2
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/220,908
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/905,846 CURRENT FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IOR APPLICATION NUMBER: US 60/265,358 IOR FILING DATE: 2001-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IOR FILING DATE: 2001-07-13
IOR APPLICATION NUMBER: US 60/291,722
IOR FILING DATE: 2001-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/905,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: GB 0108730.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-04-06
APPLICATION NUMBER: GB 0120679.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB 0030647.2
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Patent No. US20020102707A1
                                                                                                                          606 GTTCGCCATCCAATCCATC 624
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APPLICANT: Peter Stacey
APPLICANT: Roderick Thomas Walsh
                                                                                                 1 GTTCGCCATCCAGTCCATC 19
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EQ ID NO 4
LENGTH: 2893
Ouery Match 91.6%;
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-08-24
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Best Local Similarity
Matches 18; Conserva
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us-09-647-780a-20.rnpb

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NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
     SEO ID NO 4649
LEBOTH: 558
TYPE: DNA
ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISHIKAWA, JUN
HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAKAKI, YOSHIYUK
                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                 ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(558)
US-10-156-761-4649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: OLSON, ERIC
APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
FILE REFERENCE: MYOG:028US
CURRENT APPLICATION NUMBER: US/09/908,988B
CURRENT FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                               Length 2975;
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                                                                                                                                                                               DB 10;
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                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.4;
Pred. No. 56
PRIOR FILING DATE: 2000-07-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2975
                                                                                                                                                                               Score 17.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT: SHIBA, TADAYOSHI
PPLICANT: SAKKI, YOSHIYUKI
PPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
ILE REFERENCE: 249-262
                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4649, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09908988B Patent No. US20020127690A1
                                                                                                                                                                                                                                                                            2439 GTTCGCCATCCAATCCATC 2457
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                                                                                                                                                                           91.68;
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Best Local Similarity 94.4%;
Matches 17; Conservative
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HORIKAWA, HIROSHI
                                                                                                                                                                                             Best Local Similarity 94.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (199)..(1296)
US-09-908-988B-1
                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
US-09-905-846-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mus musculus
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US-09-908-988B-1
                                                                                                                                                                             Query Match
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DB 9; Length 558; 90;
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
        Score 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FLILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2051, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5690362 CGCCATCCAGTCCATC 5690347
                                                                                                                                                                                                                                       Sequence 1, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.2%;
                                                                                                             216 CGCCATCCAGTCCATC 201
      84.28;
                                                                                         4 CGCCATCCAGTCCATC 19
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Length 1194;
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APPLICANT: Meyers, Rachel A.
APPLICANT: Williamson, Mark
TITLE OF INVENTION: 32113, A NOVEL FUCOSYLTRANSFERASE FAMILY
FILLE REFERENCE: 10448-048001
CURRENT APPLICATION NUMBER: US/09/844,948
CURRENT FILING DATE: 2001-04-24
PRIOR PAPLICATION NUMBER: US 60/200,604
PRIOR FILING DATE: 2000-04-28
                                                                                                                            Score 15.8; DB 10;
Pred. No. 1.1e+02;
0; Mismatches 2;
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Pred. No. 1.1e+02;
0; Mismatches 2;
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FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
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PPLICANT: HATTORI, MASAHIRA
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICATION NUMBER: JP 2001-204089
FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2001-272697 PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5444, Application US/10156761
Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1032 GTTCGCCTTCCAGTCCTTC 1050
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                                                                                                                                                                                                                                                                                                               429 GATCGCCATCCAGCCCATC 411
                                , ORGANISM: Bacillus licheniformis US-09-974-300-2388
                                                                                                                                                                                                                                                                        1 GTTCGCCATCCAGTCCATC 19
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                                                                                                                                    Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5%;
Matches 17; Conservative
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ISHIKAWA, JUN
HORIKAWA, HIROSHI
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NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OMURA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-844-948-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (1)..(1194)
US-10-156-761-5444
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LENGTH: 1479
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       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                   Length 477;
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APPLICANT: Xu, Jiangchun
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.504
CURRENT APPLICATION NUMBER: US/09/815,343
CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PSALSEQ for Windows Version 4.0
SEQ ID NO 386
LENGTH: 548
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APPLICANT: Berka, Randy M.

APPLICANT: Clausen, 1b Groth

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Expression

TITLE OF INVENTION: Mathods For Monitoring Multiple Gene

TITLE OF INVENTION: Mathods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

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Pred. No. 1.16
0; Mismatches
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FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 386, Application US/09815343
Patent No. US20010055596A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 GTTCGCCATCCAGTCCTC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GITCGCCATCCAGTCCATC 19
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                                                                                                                                                                                                                                                                                                                                               Query Match 83.2%;
Best Local Similarity 89.5%;
Matches 17; Conservative
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                                                                                                                                                                           ; NAME/KEY: misc_feature
; LOCATION: (1)...(477)
; OTHER INFORMATION: n =
US-09-918-995-2051
                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: n
US-09-815-343-386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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US-09-974-300-2388/c
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SEQ ID NO 2051
LENGTH: 477
                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                              FEATURE:
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Length 2446; Indels

Score 15.8; DB 9; Pred: No. 1.1e+02; 0; Mismatches 2;

83.2%;

us-09-647-780a-20.rnpb

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Search completed: July 9, 2003, 02:22:52
Job time : 124.787 secs
                                                                                                                                                                                                                                                  416 GTTCCCCATCCCGTCCATC 434
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                                                           Query Match
Best Local Similarity 89.5
Matches 17; Conservative
US-10-139-683-11
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Sequence 11

Sequence 11

Sequence 11

Sequence 11

Sequence 12

Sequence 13

Sequence 14

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APPLICANT: Cosman, David J.
APPLICANT: Anderson, Dirk M.
APPLICANT: Borges, Luis
TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
TITLE OF INVENTION: Like Receptors (LIR)
FILE REFERENCE: 2624-A
CURRENT APPLICATION WHERE: US/10/139,683
CURRENT FILING DATE: 2002-05-02
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                             Length 1479;
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                      Score 15.8; DB 9;
Pred. No. 1.1e+02;
0; Mismatches 2;
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1.1e+02;
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Pred. No. 1.1e-
0; Mismatches
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PRIOR APPLICATION NUMBER: 09/310,463
PRIOR FILING DATE: 1999-05-12
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PRIOR FILING DATE: 1997-04-24
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 2446
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Publication No. US20030060614A1
GENERAL INFORMATION:
                                                                                                                                                                                                      951 GTTCGGCATCCAGTCCCTC 933
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                  Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity 89.5%;
Matches 17; Conservative
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; LOCATION: (171)...(1040)
US-10-139-662-11
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LOCATION: (171)..(1040)
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ORGANISM: human
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ORGANISM: human
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6 561 13 6 576 10 6 704 12 6 704 12 5 661 17 5 661 17 3 255 9 3 255 9 3 3 303 10 3 3 303 10 3 3 301 12 3 3 301 12	4 86.3 375 9 AL777580 4 86.3 439 14 BA613878 8 86.3 456 10 BE099923 4 86.3 461 9 AV006036 4 86.3 485 11 AK19655 4 86.3 571 17 BH216223 4 86.3 571 17 BH216223 4 86.3 628 12 BF284900	4 86.3 638 95 4 86.3 659 14 86.3 659 14 86.3 669 13	6.3 991 17 CNSGSQZF AL348720 4.2 207 14 BQ820536 BQ820536 4.2 325 13 B1725875 B1725875 4.2 325 13 B0726030 B0725875 4.2 325 13 B0726030 B0725875 4.2 402 14 BQ81766 BM000030 4.2 461 10 BE444566 BE405532 4.2 494 10 BE444568 BG846660 4.2 520 14 BQ819945 BQ819945	ALIGNMENTS BE106100 UI-R-B01-ask-h-09-0-UI.s1 UI-R-B01 Rattus norvegicus CDNA clone UI-R-B01-ask-h-09-0-UI 3', mRNA sequence. BE106100 BE1061001 GI:8498202	gicus letazoa; Chordat theria; Rodenti to 507) Lennon,G. and and subtracti	Genome kes. b (9), 791 800 (1990) 97044477 Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 761: 319 335 9565 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A
000000000000000000000000000000000000000			0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 BE106100/C LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	ADORNAL MEDITINE COMMENT
n 5.1.6 Compugen Ltd. cearch time .963.254 Seconds (without alignments) 319.453 Million cell updates/sec	20200120	3,2308134		*	cted by chance to have a of the result being printed, score distribution.	Description BE106100 UI-R-B01- BE987421 MR3-G0015 AW924814 WS1_72_C0 AW745327 WS1_33_G0 BF446399 7p56907.x* BF437289 7p69f03.x
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. nucleic search, using sw model July 8, 2003, 00:47:28; Search time 963. 319.453 Million		Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	STS	10. gb_est2:* 11. gb_htc:* 12. gb_est3:* 13. gb_est3:* 14. gb_est5:* 15. em_est4:* 16. em_est6m:* 17. gb_gss.* 18. em_gss_hum:* 19. em_gss_hum:* 20. em_gss_ph:*	em_gss_fun: em_gss_mam:* em_gss_mus:* em_gss_pro:* em_gss_rod:* the number of results predi than or equal to the score ed by analysis of the total	SCORE MATCH Length DB ID 19 100.0 507 10 BE106100 17.4 91.6 351 12 BE987421 17.4 91.6 524 10 AW745327 17.4 91.6 530 12 BF446399 17.4 91.6 554 12 BF445399

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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W.Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolivekir, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF987421 351 bp mRNA linear EST 23-JAN-2001 MR3-GN0150-101000-002-c07 GN0150 Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pryT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The library (UI-R-B01) is a subtracted library derived from a mixture of the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized medulla library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Baboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                /clone="UI-R-B01-ask-h-09-0-UI"
/clone_lib="UI-R-B01"
                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                  /strain=!Sprague-Dawley
                                                                                                                                                                                                                                                                                        'db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                   'dev_stage="adult"
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133 c 15
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BF987421.1 GI:12393743
                                                                                                                                 Seq primer: M13 Forward POLYA-Yes.
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Fax: +55-11-2707001
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BF987421/c
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/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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                          /scripts/gethtml2.pl?t1=MR3&t2=MR3-GN0150-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
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Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bloinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 351;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
clade; Panicoideae; Andropogoneae; Sorghum.
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from Sorghum: water-stressed plants
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Pred. No. 9.6e+02;
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154 c 172 g 73
                     (http://www.ludwig.org.br/scripts/
101000-002-c07613=2000-10-10644-1)
Seg primer: puc 18 forward
High quality sequence start: 32
High quality sequence stop: 351.
Location/Qualiflers
                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="GN0150"
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High quality sequence stop: 479
POLYA-No.
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Matches 18; Conservative
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Fax: 706 583 0210
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AW924814/C
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91.68;
94.78;
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        Homo sapiens
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/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zāp; Site_1: XhoI;
Site_2: EcorR; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

174 c 174 g 81 t
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                                                                                                                                                                                                          EST 19-JUL-2000
                                                                                                                                                                                                                                                                                                                                          Eukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to exclude PolyA, vector and regions threshold for highest quality sequence
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WS1_33_G01.b1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 524;
                           Score 17.4; DB 10; Length 481; Pred. No. 1.1e+03;
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Pred. No. 1.1e+03;
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/db_xref="taxon:4558"
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below Phred quality 16. The
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                                                                                            . 1 GTTCGCCATCCAGTCCATC 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mmpratt@uga.edu
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ilarity 94.7%;
Conservative
                              91.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer; JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 706 542 1860
Fax: 706 583 0210
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                Sorghum bicolor
                                                                                                                                                                                                                                               mRNA sequence.
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BF446399
BF446399.1
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Matches 18; Conserv
                                               Similarity
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                                                                 18;
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AW745327/c
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JOURNAL
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circles were made in vitro Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "a 146 c 191 g 101 t lothers
                                                                                                                                                                                                                                                        Email: cgapbs r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF437289 554 bp mRNA linear EST 29-NOV-2000 7p69f03.x1 NCI_CGAP_PT28 Homo sapiens cDNA clone IMAGE:3651197 3' similar to TR:Q9QZV6 Q9QZV6 SOLUBLE SECRETED ENDOPEPTIDASE DELTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 530)
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Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pT7T3D-Pac (Pharmacia)
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Pred. No. 1.1e+03;
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                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 466
Location/Qualifiers
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BF437289
BF437289.1 GI:11449622
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/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                             125 GGTCGCCATCCAGTCCATC 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 706 542 1860
Fax: 706 583 0210
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Matches 18; Conserv
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BE355985
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BE355985/c
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BE594778/c
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KEYWORDS
SOURCE
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CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University, Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: infocemage.llnl.gov
Seg primer: -400P from Gibco
High quality sequence stop: 462.
                                                                                                                                                                                                                                                                                                                                               /note="Organ: prostate; Vector: pr773D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615)
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG933273 561 bp mRNA linear EST 07-JUN-
WS1_92_D06.91_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
mRNA sequence.
BG933273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Bullding, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 554;
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0; Mismatches 1
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    .561
    /organism="Sorghum bicolor"

                                                                                                                                                                                                                                              clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                           quality sequence stop: 462.
Location/Qualifiers
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Contact: Cordonnier-Pratt MM
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/lab_host="DH10B"
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94.78;
                                                                                                                                                                                                                                                                                        sex="male"
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Matches 18; Conservative
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BG933273/c
LOCUS
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AUTHORS
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COMMENT
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/clone_lib="Water-stressed 1 (WS1)"
.wote="Organ: Mix of 5-week old plants on days 7 & 8 after
.water was withheld; Vector: Lambda Zap; Site_1: XhoI;
Site_2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass exclsion."
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1 (bases 1 to 576)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
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/db xref="taxon:4558"
/clone_lib="park Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_l: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZaP II.
Clones to be sequenced were prepared by mass excision."
a 178 c 203 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE355985 576 bp mRNA linear EST 20-JUL-200
DG1_121_C06.bl_A002 Dark Grown 1 (DG1) Sorghum bicolor CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                 Gaps
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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                                                                                                                                                                                                                                                                             Length 561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An EST database from Sorghum: dark-grown seedlings
                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                             Ouery Match 91.6%; Score 17.4; DB 13; Best Local Similarity 94.7%; Pred. No. 1.1e+03; Matches 18; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17.4; DB 10;
Pred. No. 1.1e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 511 POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Euteleostomi;

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

COMMENT

LOCUS DEFINITION

ACCESSION

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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library
Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  вназоизта 661 bp DNA linear GSS 03-DEC-2001
CH230-32012.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-32012, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mämmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           //dev_stage="embryo"
//dev_sta
                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap...
National.Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleost
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 704;
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Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .704
/organism="Rattus norvegicus"
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9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         info@image.llnl.gov
Seq primer: -400p from Gibco
High quality sequence stop: 422.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10116"
/clone="IMAGE:4176045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_GSSs: CH230-32012.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.6%;
ilarity 94.7%;
Conservative
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                                                                                                                                                                                                                                        (bases 1 to 704)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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Unpublished (1997)
                                                                            norvegicus
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Best:Local Similarity
Matches 18; Conserv
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ORIGIN
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AUTHORS
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JOURNAL
                                                                                ORGANISM
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                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
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KEYWORDS
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1. 592
/organism="Sorginum bicolor"
/db_xref="taxon:4558"
/clone_lib="Pathogen induced 1 (PII)"
/clone_lib="Pathogen induced 1 (PII) (PII) (PII) (PII)
/clone_lib="Pathogen induced 1 (PII) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           grow older (4 weeks or older), plants resume susceptibility to anthracnose disease. The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision, WARNING: While
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 05-FEB-2001
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BG153322 G1:12665352
    EST 18-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   most or all ESTs are expected to derive from the host plant, no effort was made to eliminate ESTs deriving from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                 Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seedlings 48 hours after inoculation. Note: young seedlings (2 weeks old) exhibit juvenile resistant reaction, which is an incompatible interaction. As they
    592 bp mRNA linear EST 18-AUG-20.gl_A002 Pathogen induced 1 (P11) Sorghum bicolor CDNA,
                                                                                                                                                                                                                                                                                               Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae; PACC
clade; Panicoldeee; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Pred. No. 1.1e+03;
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High quality sequence stop: 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209 GGTCGCCATCCAGTCCATC 191
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                                                                                                                                                                             GI:9849851
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ilarity 94.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra, M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Worbh, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., More, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="Vector: pBluescript SK+; Site_1: XbaI; Site_2: XhoI
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availabliity, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMMGE Consortium (info@image.llnl.gov) for further information. MGI:520743.
                                                                                                                                                                                                                                                                                                               /cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoR1; Site_2: EcoF
CHORI-230 Rat (BN/SSNHsd/MCW) BAC library produced by
Pieter de Jong"
                                                                       Gaps
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/strain="C57BL/6J x DBA/2J F1"
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cloned unidirectionally from mRNA prepared from primitive streak embryonic tissue. Primer: Oligo dr. cDNAs were cloned into the Xbal/Xhol sites of pBluescript SK+ (Strangaene) using commercial linkers (NEB). Average insert size: 0.5 kb. "
11 insert size: 0.5 kb."
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Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&t2=MR4-RT0045-
250401-008-c05&t3=2001-04-25&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 73
High quality sequence start: 73
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 291)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/db_xref="taxon:9606"
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/dev_stage="Adult"
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llarity 94.4%;
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Chordata; Craniata; Vertebrata; Euteleostomi;

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Catarrhini; Hominidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-HT0165-060
200-007-cl2&t3=2000-02-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 182.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, sao Paulo-SP,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.6e+03;
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/clone_lib="HT0165"
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